

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2005, 16:44:00 ; Search time 4555 Seconds
(without alignments)
10956.942 Million cell updates/sec

Title: us-10-089-278-1
Perfect score: 1030
Sequence: 1 tccaccactctgactcaag.....ccagccagtcagtttatc 1030

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
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4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1030	100.0	1030	6	AX111694	AX111694 Sequence
2	644	62.5	990	6	AX111696	AX111696 Sequence
3	629.2	61.1	946	6	AX111697	AX111697 Sequence
4	598.8	58.1	927	6	AX111695	AX111695 Sequence
5	564.6	54.8	1632	12	SYN507107	AJ507107 Synthetic
6	544.4	52.9	1695	12	SC0544530	AJ544530 Synthetic
7	542.4	52.7	744	12	AF402256	AF402256 Synthetic
8	538	52.2	2190	6	AX100186	AX100186 Sequence
9	537.6	52.2	876	6	AX100194	AX100194 Sequence
10	537.4	52.2	969	6	AX100188	AX100188 Sequence
11	524	50.9	795	10	MMSCFVP25	Z70662 Artificial
12	522.6	50.7	925	6	E30617	E30617 Antibody an
13	508.4	49.4	687	12	AF003707	AF003707 Synthetic
14	505	49.0	1817	6	AX739887	AX739887 Sequence
15	497.6	48.3	882	12	SC0278109	AJ278109 Synthetic
16	496.2	48.2	687	12	AF003705	AF003705 Synthetic
17	487.6	47.3	897	6	CQ881538	CQ881538 Sequence
18	486	47.2	1314	6	A68604	A68604 Sequence 4
19	483	46.9	993	6	AX798477	AX798477 Sequence

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21	482.2	46.8	1698	6	AX011206	AX011206 Sequence
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26	474.2	46.0	4354	12	ASY14583	Y14583 Artificial
27	471	45.7	732	12	AY725472	AY725472 Synthetic
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30	460.4	44.7	1906	6	AX777477	AX777477 Sequence
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33	457	44.4	1653	6	AX011208	AX011208 Sequence
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39	447.8	43.5	747	6	AX100178	AX100178 Sequence
40	447	43.4	1817	6	AX739885	AX739885 Sequence
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ALIGNMENTS

RESULT 1
AX111694

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

AX111694
Sequence 1 from Patent WO0125415.

AX111694

AX111694.1 GI:13927959

synthetic construct

synthetic construct

other sequences; artificial sequences.

1

Cichutek, K. and Engelstaedter, M.

Gene transfer in human lymphocytes using retroviral scfv cell

targeting

Patent: WO 0125415-A 1 12-APR-2001;

Bundesrepublik Deutschland LET (DE)

Location/Qualifiers

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/organism="synthetic construct"

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/db_xref="taxon:32630"

/note="scFv kodierende Sequenz"

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Query Match

Best Local Similarity

Matches 1030; Conservative

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QY

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QY

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QY

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QY

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Db 301 GAGTCATGCAAGAGTCTGAGTGGATTGACATTTATTTAGTACTTACTATGTTGATCCTAG 360

QY 361 TTACAACAGAGGTTCAAGGGCAAGGCCAACATGACTGTAGACAAATCTCTCAACACAGC 420

Db 361 TTACAACAGAGGTTCAAGGGCAAGGCCAACATGACTGTAGACAAATCTCTCAACACAGC 420

QY 421 CTATTTGGAACTTCCAGACTGACATCTGAGGATTCGCCATTTATTTGTCAGATC 480

Db 421 CTATTTGGAACTTCCAGACTGACATCTGAGGATTCGCCATTTATTTGTCAGATC 480

QY 481 GGATGGTAATTTACGGGTATTACTATGCTTTGGACTACTGGGGCCAAAGGCCACTACGGTCA 540

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Db 1021 CCAGTTTATC 1030

RESULT 2

AX111696

LOCUS AX111696 990 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 3 from Patent WO0125415.

ACCESSION AX111696

VERSION AX111696.1 GI:13927961

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 Cichutek, K. and Engelstaedter, M.

AUTHORS Gene transfer in human lymphocytes using retroviral scfv cell

TITLE targeting

JOURNAL Patent: WO 0125415-A 3 12-APR-2001;
Bundesrepublik Deutschland LET (DE)

FEATURES

source Location/Qualifiers

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/note="scFv kodierende Sequenz"

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QY 104 CTAATTTCTCTTGTGGCTTGTGGGGTGTGGGACCACTGCCGAAGTTTCGACTGCCGA 163

Db 61 CTAATTTCTCTTGTGGCTTGTGGGGTGTGGGACCACTGCCGAAGTTTCGACTGCCGA 120

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QY 224 CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTCTGGCTACACATTCAGTATTTAGT 283

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QY 344 TACTATGTGATCTAGTTTACAAACAGAGGTTCAAGGGCAAGGCCAATAGCTGTAGAC 403

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QY 404 AATCTCTCAACACAGCTTATTTGGAACTTGGCACTGACATCTCAGAGTCTGCCATT 463

Db 361 AATCTCTCAGTACAGCTTACGCACTGACAGCTGACATCTGAGGACTCTGAGCTC 420

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Db 469 CAAGGCACTACGGTCAACCGTCTCTCAGGTGAGGCGGTTTCAAGGCGGAGGTGGCTCTGGC 528

QY 584 GGTGGCGGATCGGATATCGAGCTCACTCAGTCTCCATCTCTTTGGCTGTCTCTAGGG 643

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QY 764 AACCTAGAACTCGAGTCTCTGCGAGGTTCAAGTGGAGTGGGTCTCAGTCAAGACTTCAC 823

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Db 754 CTCACCAATCAGCCGAATGGAGGCTGAAGATGCTGCCACTATTACTGCCCAAGAGAGT 813

QY 884 GAAGATCCGTACAGTTCGGAGGGGACCAAGCTGGAATATAAAGCGGGCGGCGATCCG 943

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RESULT 3
AX111697
LOCUS AX111697 946 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 4 from Patent WO0125415.
ACCESSION AX111697
VERSION AX111697.1 GI:13927962
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cichutek, K. and Engelstaedter, M.
TITLE Gene transfer in human lymphocytes using retroviral scfv cell
JOURNAL targeting
Patent: WO 0125415-A 4 12-APR-2001;
Bundesrepublik Deutschland LET (DE)
FEATURES
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QY 944 GGCTCCGGGGCGGTGTTCTGCTGGTGGTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1001
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RESULT 4
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LOCUS AX111695 927 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 2 from Patent WO0125415.
ACCESSION AX111695
VERSION AX111695.1 GI:13927960
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cichutek, K. and Engelstaedter, M.
TITLE Gene transfer in human lymphocytes using retroviral scfv cell
JOURNAL targeting
Patent: WO 0125415-A 2 12-APR-2001;
Bundesrepublik Deutschland LET (DE)
FEATURES
Location/Qualifiers
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Best Local Similarity 78.6%; Pred. No. 6.5e-152;
Matches 755; Conservative 0; Mismatches 172; Indels 33; Gaps 2;

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QY 224 CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTCTTGGCTACACATTCATGATTATGTT 283
Db 181 CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTCTTGGCTACACATTCATGATTATGTT 240

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Db 1037 ATGGGAAGTTCAAGGGCAAGGCCACCACTGACTGCAGACAAATCCTCCAGCACAGCCTACA 1096
QY 426 TGGAACTGCGACACTGACATCTGAGGATTCGCGCATTTATTATTATGTCGAAGATCGGATG 485
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QY 906 GGGGACCAAGCTGGAATAAAACGGGCGGCCGCA 940
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RESULT 6
SC0544530
LOCUS
DEFINITION
Synthetic construct for anti-CD95 and anti-HMWG scFv antibody,
clone r95M.
ACCESSION
AJ544530
VERSION
AJ544530.1 GI:28804184
KEYWORDS
antibody; heavy chain; immunoglobulin; light chain; scFv; variable
region.
SOURCE
synthetic construct
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 1695)
AUTHORS
Grosse-Hovest,I.
TITLE
Direct Submission
JOURNAL
Submitted (14-FEB-2003) Grosse-Hovest L., Immunology, University of
Tuebingen, Auf der Morgenstelle 15, 72076 Tuebingen, GERMANY
FEATURES
Location/Qualifiers
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1222..1266
/notes="linker sequence"
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/products="immunoglobulin light chain variable region"

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Best Local Similarity 83.6%; Pred.No.4.6e-137;
Matches 630; Conservative 0; Mismatches 121; Indels 3; Gaps 1;
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Db 860 AGGTGAAGCTGCAGCAATCTGGACCTGTGGTGGTGAAGCCTGGGGCTCTCAGTGAAGATTT 919
QY 246 CCTGCAAGGTTCTGGCTACACATTCACCTGATTATGCTATGCTGGTGAACACAGATC 305
Db 920 CCTGCAAGGTTCTGGCTACGCAATTCAGTAGGTCTTGGATGAACCTGGTGAACAGAGGC 979
QY 306 ATGCAAGAGTCTAGAGTGGATTTAGTACTTATTAGTACTTACTACTGATCTCTAGTTACA 365
Db 980 CTGGACAGGGTCTTGAGTGGATTTGGACGGATTTATCTCTGGAGATGGAGATACTAATCA 1039
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QY 366 ACCAGAGTTTCAAGGGCAAGCCACAAATGACTGTAGACAAATCCTCCAAACACAGCCTATT 425
Db 1040 ATGGGAAGTTCAGGGCAAGCCACAACTGACTGTCACAAATCCTCCAGCAGACCTACA 1099
QY 426 TGGAACTTGCAGACTGACATCTGAGGATTTCCCAATTTATTATTGTGCAAGATCGGATG 485
Db 1100 TGCAGGTTCAGCAGCCTGACCTCTGTGGACTCTCGGTCTATTCTGTGCAAGAGGAA-- 1157
QY 486 GTAATTACGGGTATTACTATGCTTTTGGAATACTAGTGGGGCCCAAGGCATAAGTCCACGTCT 545
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QY 546 CCTCAGGTGAGCGGTTTCAAGCGGAGGTGGCTCTGCGGTGGCGATCGGATATCGAGC 605
Db 1217 CCTCAGGTGAGCGGTTTCAAGCGGAGGTGGCTCTGCGGTGGCGATCGGATATCGAGC 1276
QY 606 TCACTCAGTCTCCATCTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCTCTGCA 665
Db 1277 TCACTCAGTCTCCAGCTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCTCTGCA 1336
QY 666 GAGCCAGTGAAGTGTGATAGTATGGCGATAGTATTATGCACTGGTATCAGCAGAAAC 725
Db 1337 GAGCCAGTGAAGTGTGATAGTATGGCGATAGTATTATGCACTGGTATCAGCAGAAAC 1396
QY 726 CAGGACAGCCACCAAACTCCTCATCTATCGTGCATCCAACTAGAAATCTGGAGTCCCTG 785
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QY 846 AAGATGATCTGTCAGTGTATTACTGTCTGCAAGTATGGAGATCCGTACACGTTGGAG 905
Db 1517 CTGATGATCTGTCAGTGTATTACTGTCTGCAAGTATGGAGATCCGTACACGTTGGAG 1576
QY 906 GGGGGACCAAGCTGGAAATAAAACGGGGCGCGC 939
Db 1577 GGGGGACCAAGCTGGAGCTGAAGAGACAGTGGC 1610
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RESULT 7
AF402256 LOCUS
DEFINITION Synthetic construct single chain antibody HFN7.1 mRNA, partial cds.
ACCESSION AF402256
VERSION AF402256.1 GI:15149452
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 744)
Kassner,P.D.
Direct Submission
Submitted (24-JUL-2001) Molecular Biology, Pointilliste, 2541
Leghorn Street, Suite #4, Mountain View, CA 94043, USA
JOURNAL
FEATURES
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1..744
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/db_xref="taxon:32630"
/notes="derived from Mus musculus hybridoma"
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Best Local Similarity 83.7%; Pred. No. 1.5e-136;
Matches 628; Conservative 0; Mismatches 116; Indels 6; Gaps 1;
QY 179 ATGGCCGAGGTCAAGCTGCAGCAGTCAGGGGCTGAGCTGAGCTGAGGCTCGGGTCTCAGTG 238
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QY 239 AAGATTTCCTGCAAGGGTTCTGGCTACACATTCACCTGATTTATGGTATGAGCTGGGTGAA 298
Db 61 AAGATGCTCTGCAAGGGTTCTGTATACACATTCACCTGACTATGTTATAAGCTGGGTGAAG 120
QY 299 CAGAGTCATGCAAAAGTCTAGAGTGGATGAGCTTATAGTACTTACTATGATGATCCT 358
Db 121 CAGAGAACTGGACAGGGCTTGAAGTGGATTGAGAGATTTATCCTGGAAAGTGGTAGTACT 180
QY 359 AGTTACAAACAGAGGTTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCTCTCAACACA 418
Db 181 TACTACATAGAGATTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCTCTCAACACA 240
QY 419 GCCTATTTTGGAACTTCCAGACTGACATCTGAGGATTTCTGCCATTTTATTTGTGCAAGA 478
Db 241 GACTACATCAGCTCAGCAGCCTGACATCTGAGGACTCTCGGTCTATTCTCTGTGCAAGA 300
QY 479 TGGATGTTAATTAACGGGTATTACTATGCTTTGGACTACTGGGGCCCAAGGCACTAGGTC 538
Db 301 AGGAGGGGTAAACAAC-----TCTTATGCTATGAGACTACTGGGGCCCAAGGCACTAGGTC 354
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Db 415 ATCGAGCTCAGTCTCCAGCTCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACATC 474
QY 659 TCTGAGAGCCAGCAGTAAAGTGTGATAGTTATGCGGATAGTTTATGCACTGGTATCAG 718
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QY 719 CAGAAACAGGACAGCCACCCAAACCTCTCATCTATCGTGCATCCCAACCTAGAAATCTGGA 778
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QY 839 GTGGAGAGATGATGCTGCTCAGTGTATTACTCTCTCAAGTATGGAAGTATCGGTACACG 898
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Db 715 TTCCGTTGGAGCCCAAGCTGGAAATCAAA 744
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RESULT 8
AX100186 LOCUS
DEFINITION Sequence 93 from Patent WO0119992.
ACCESSION AX100186
VERSION AX100186.1 GI:13539105
PAT 02-APR-2001
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Db 610 CCCAACTCTCATCTATCTTGCATCCAACTAGATCTGGGTCCTGCCAGGTTCACT 669
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Qy 857 GCAGTGTATTACTGTCTGCAAGTATGGAAGATCCGTACACGTTCCGAGGGGGACCAAG 916
Db 730 GCAACCTATTACTGTGAGCAGATAGGAGCTTCTCGGACGTTCCGTGGAGGCCACCAAG 789
Qy 917 CTGGAATAAAGCGGGCGCGCA 940
Db 790 CTGGAATCAAGCGGGCGCGCA 813

RESULT 10
AX100188
LOCUS AX100188
DEFINITION Sequence 95 from Patent WO0119992.
ACCESSION AX100188
VERSION AX100188.1 GI:13539106
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 Scheiflinger, F., Kerschbaumer, R., Falkner, F. G. and Dörner, F.
AUTHORS Factor ix/factor ixa antibodies and antibody derivatives
TITLE Patent: WO 0119992-A 95 22-MAR-2001;
JOURNAL Baxter Aktiengesellschaft (AT)
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Query Match 52.2%; Score 537.4; DB 6; Length 969;
Best Local Similarity 80.2%; Pred. No. 3.6e-135;
Matches 647; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

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Db 19 ACGCAGCCGCTGGATTGTTTACTTCGCGGCCAGCGGCCCATGGCGAGGTTCAAGCTT 78
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Qy 257 TCTGGCTACACATCACTGATTATGGTATGATGCGGTGAACAGAGTCAATGCCAAAGT 316
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Db 199 CTTGAGTGGATTGACCGGATTTATCTGGAAATGGAGATTAACATACATGGGAAGTTTC 258
Qy 377 AAGGGCAAGGCCCAATGACTGTAGACAAATCTCTCCAAACAGACCTATTTGGAACCTTGC 436
Db 259 AAGGGCAAGGCCCACTGACTGTCAGACAAATCTCTCCAGCACAGCTACATGCAGCTCAGC 318
Qy 437 AGACTGACATCTGAGGATCTGCGATTATATTTGTCAGATCGGATGATTAATACGGG 496
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Qy 497 TATTACTATCTTTGGACTACTGGGGCAAGGCACTACGGTCAACCGTCTCCTCAGGTGGA 556
Db 370 TATTACTATCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGGTGGA 429
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Qy 917 CTGGAATAAAGCGGGCGCGCATCG 943
Db 790 CTGGAATCAAGCGGGCGCGCACCG 816

RESULT 11
MMSCFVP25
LOCUS MMSCFVP25
DEFINITION Artificial mRNA for single chain antibody scFv (scFVP25).
ACCESSION Z70562
VERSION Z70562.1 GI:1360013
KEYWORDS heavy chain; light chain; single chain antibody; variable region.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 795)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Fecker, L., Kaufmann, A., Commandeur, U., Reither, J., Koenig, R. and
Burgermeister, W.
Expression of single chain antibody fragments (scFv) specific for
beet necrotic yellow vein virus structural and nonstructural
proteins in Escherichia coli and Nicotiana benthamiana
Unpublished
2 (bases 1 to 795)
Fecker, L.
Direct Submission
Submitted (03-APR-1996) Fecker L., Biologische Bundesanstalt fuer
Land- und Forstwirtschaft, Institut fuer
Biochemie/Pflanzenvirologi, Messeweg 11-12, Braunschweig, Germany,
38104
FEATURES
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RESULT 13
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LOCUS
DEFINITION
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  partial cds.
ACCESSION
  AF003707
VERSION
  AF003707.1 GI:3322218
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  synthetic construct
SOURCE
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  other sequences; artificial sequences.
REFERENCE
  1 (bases 1 to 687)
  Amerdorfer,P., Wong,C., Chen,S., Smith,T., Deshpande,S.,
  Sheridan,R., Finnern,R. and Marks,J.D.
  Molecular characterization of murine humoral immune response to
  botulinum neurotoxin type A binding domain as assessed by using
  phage antibody libraries
  Infect. Immun. 65 (9), 3743-3752 (1997)
JOURNAL
  MEDLINE
  PUBMED
  9284147
REFERENCE
  2 (bases 1 to 687)
  Amerdorfer,P.
  Direct Submission
  Submitted (13-MAY-1997) Anesthesia, University of California at San
  Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
  3 (bases 1 to 687)
  Amerdorfer,P.
  Direct Submission
  Submitted (16-JUL-1998) Anesthesia, University of California at San
  Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
  Sequence update by submitter
REMARK
  On Jul 16, 1998 this sequence version replaced gi:2306928.
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CDS
  Query Match 49.4%; Score 508.4; DB 12; Length 687;
  Best Local Similarity 83.8%; Pred. No. 2.8e-127;
  Matches 625; Conservative 0; Mismatches 61; Indels 60; Gaps 2;

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QY 366 ACCAGAGGTTCAAGGGCAAGGCCACAAATGACTGTAGACAAATCCTCCAAACAGACCTATT 425
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Db 242 TGGAACTGCCAGACTGACATCTGAGGATTCGCCATTTATTATTGTGCAAGATCGGATG 294

QY 486 GTAAATTACGGGTATTACTATGCTTTGGACTACTTGGGGCCAAAGCACTACGGTCAACGCT 545
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QY 726 CAGGACAGCCCAACCAACTCTCATCTATCGTGCATCCAACTAGAAATCTGGAGTCCCTG 785
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QY 906 GGGGGACCAAGCTGGAAATAAAACGG 931
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RESULT 14
AX739887
LOCUS
DEFINITION
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ACCESSION
  AX739887
VERSION
  AX739887.1 GI:30519176
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
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  le Gall,F., Kipriyanov,S., Reusch,U., Moldenhauer,G. and Little,M.
  Dimeric and multimeric antigen binding structure
  Patent: WO 03025018-A 25 27-MAR-2003;
  Affimed Therapeutics AG (DE)
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[illegible]

RESULT 15
SCO278109
LOCUS
DEFINITION

GenCore version 5.1.6
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Run on: August 23, 2005, 16:40:35 ; Search time 616 Seconds

(without alignments)
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Title: US-10-089-278-1

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	537.6	52.2	876	4	AAF30734
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16	483	46.9	993	9	AAU56799
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ALIGNMENTS

RESULT 1

AAF61509

ID AAF61509 standard; DNA; 1030 BP.

XX AAF61509;

AC AC

DT 11-SEP-2003 (revised)

DT 25-JUN-2001 (first entry)

XX

DE DNA encoding SNV-env leader/human 7AS-scFv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;

KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;

KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;

KW acquired immune deficiency syndrome; severe combined immune deficiency;

KW T cell lymphoma; fusion construct; ds.

XX Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX

XX Key Location/Qualifiers

FT CDS 44..178

FT /*tag= a

FT /product= "SNV-env leader peptide"

FT /note= "No stop codon given"

FT CDS 179..1030

FT /*tag= b

FT /product= "7AS-scFv"

FT /note= "no stop codon given"

FT /partial

XX DE19946142-A1.

PN 29-MAR-2001.

XX 27-SEP-1999; 99DE-01046142.

XX 27-SEP-1999; 99DE-01046142.

PR (BUND) BUNDESREPUBLIK DEUT PAUL-BHRLLICH-INST.

XX Cichutek K, Engelstaedter M;

XX

XX WPI: 2001-246140/26.
DR P-PSDB; AAB70840.
XX
PT Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT variable antibody fragment.
XX
PS Claim 1; Fig 1; 19pp; German.
XX
CC This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (1) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and Hela (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transformation. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for Hela,
CC showing the high selectivity for human T cells. This sequence encodes the
CC SNV-env leader/human 7A5-scFv fusion construct used in the construction
CC of novel cell targeting vectors described in the invention. (Updated on
CC 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 1030 BP; 232 A; 244 C; 304 G; 250 T; 0 U; 0 Other;

Query Match 100.0%; Score 1030; DB 5; Length 1030;
Best Local Similarity 100.0%; Pred. No. 4.8e-249;
Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCACCACTCTCGACTCAAGAAAGCTCTCACCAACCAAGAAATGGACTGTCTCACCAA 60
DB 1 TCCACCACTCTCGACTCAAGAAAGCTCTCACCAACCAAGAAATGGACTGTCTCACCAA 60
QY 61 CCTCCGATCCGCTGAGGGTAAAGTTGACACGCGGAGCAAAATCCTAATTCCTCTGTGGC 120
DB 61 CCTCCGATCCGCTGAGGGTAAAGTTGACACGCGGAGCAAAATCCTAATTCCTCTGTGGC 120
QY 121 TTGGTGGGGGTTTGGGACCACTGCCGAAGTTTCGACTGCCGCGGAGCGCCAGCGGCCAT 180
DB 121 TTGGTGGGGGTTTGGGACCACTGCCGAAGTTTCGACTGCCGCGGAGCGCCAGCGGCCAT 180
QY 181 GGCGGAGGTCAAGCTGCAGCAGTCAGGGGCTGAGCTGGTGAGCGCTGGGGTCTCAGTGAA 240
DB 181 GGCGGAGGTCAAGCTGCAGCAGTCAGGGGCTGAGCTGGTGAGCGCTGGGGTCTCAGTGAA 240
QY 241 GATTTCCTGCAAGGGTTCTGGCTACACATTCACCTGATATGTTATGAGCTGGGTGAAACA 300
DB 241 GATTTCCTGCAAGGGTTCTGGCTACACATTCACCTGATATGTTATGAGCTGGGTGAAACA 300
QY 301 GAGTCATGCAAGAGTCTAGAGTGGATTGGACTTATAGTACTTACTATGTTGATCCTAG 360
DB 301 GAGTCATGCAAGAGTCTAGAGTGGATTGGACTTATAGTACTTACTATGTTGATCCTAG 360
QY 361 TTACAACACAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCTCCCAACACAGC 420
DB 361 TTACAACACAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGACAAATCTCCCAACACAGC 420
QY 421 CTATTTGGAACTTGCCACAGCTGACATCTGAGGATTCGCCATTTATTTATTTGTCAGATC 480
DB 421 CTATTTGGAACTTGCCACAGCTGACATCTGAGGATTCGCCATTTATTTATTTGTCAGATC 480
QY 481 GGATGGTAATTACGGGTATTACTATGCTTTGGACTACTGGGCGCAAGGCACCTACGGTCAC 540
DB 481 GGATGGTAATTACGGGTATTACTATGCTTTGGACTACTGGGCGCAAGGCACCTACGGTCAC 540

QY 541 CGTCTCTCAGGTGGAGCGGTTTCAGCGGAGAGTGGCTCTGCGGTGGCGGATCGGATAT 600
DB 541 CGTCTCTCAGGTGGAGCGGTTTCAGCGGAGAGTGGCTCTGCGGTGGCGGATCGGATAT 600
QY 601 CGAGCTCACTAGTCTCCATCTTTTGGCTGTGTCTTAGGGCAGAGGGCCACCATATC 660
DB 601 CGAGCTCACTAGTCTCCATCTTTTGGCTGTGTCTTAGGGCAGAGGGCCACCATATC 660
QY 661 CTGCAGAGCCAGTGAAGGTGTGATAGTTATGGCGATAGTTTATGCACTGGGTATCAGCA 720
DB 661 CTGCAGAGCCAGTGAAGGTGTGATAGTTATGGCGATAGTTTATGCACTGGGTATCAGCA 720
QY 721 GAAACAGACAGCCAGCCCAAACTCCTCATCTATCGTGCATCCAACTAGAATCTCGAGT 780
DB 721 GAAACAGACAGCCAGCCCAAACTCCTCATCTATCGTGCATCCAACTAGAATCTCGAGT 780
QY 781 CCTGTCAGGTTCAAGTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCCTGT 840
DB 781 CCTGTCAGGTTCAAGTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCCTGT 840
QY 841 CGAGGAAGATGATGCTGCACTGTATTACTGTCTGCAAAAGTATGGAAGATCCCGTACACGTT 900
DB 841 CGAGGAAGATGATGCTGCACTGTATTACTGTCTGCAAAAGTATGGAAGATCCCGTACACGTT 900
QY 901 CGAGGGGGGACCAAGCTGGAATAAAGCGGCGCGCATCGGGCTCCGGGGCGGTGG 960
DB 901 CGAGGGGGGACCAAGCTGGAATAAAGCGGCGCGCATCGGGCTCCGGGGCGGTGG 960
QY 961 TTCTGTTGTTGGTTCCTGTTGGTGGTGGTTCCTGTTGGTGGTGGTTCCTGTTGGGCGCCAGT 1020
DB 961 TTCTGTTGTTGGTTCCTGTTGGTGGTGGTTCCTGTTGGTGGTGGTTCCTGTTGGGCGCCAGT 1020
QY 1021 CCAGTTTATC 1030
DB 1021 CCAGTTTATC 1030
RESULT 2
AAF61511
ID AAF61511 standard; DNA; 990 BP.
XX
AC AAF61511;
XX
DT 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry)
XX
DE DNA encoding SNV-env leader/human 7B2-scFv fusion construct.
XX
KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct; ds.
XX
OS Homo sapiens.
OS Spleen necrosis virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
CDS 1..135
FT /*tag= a
FT /product= "SNV-env leader peptide"
FT /note= "No stop codon given"
FT 136..990
FT /*tag= b
FT /product= "7B2-scFv"
FT /note= "no stop codon given"
FT partial
XX
PN DE19946142-A1.
XX
PD 29-MAR-2001.
XX

XX		29-MAR-2001.	
PD			
XX			
PF		27-SEP-1999; 99DE-01046142.	
XX			
PR		27-SEP-1999; 99DE-01046142.	
XX			
PA	(BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.		
XX	Cichutek K, Engelstaedter M;		
PI			
DR	WPI; 2001-246140/26.		
DR	P-PSDB; AAB70843.		
XX			
PT	Cell-targeting vector selective for T lymphocytes, useful in gene therapy		
PT	of e.g. acquired immune deficiency syndrome, encodes a single-chain		
PT	variable antibody fragment.		
XX			
XX	Claim 1; Fig 4; 18pp; German.		
XX	This invention describes a novel cell-targeting vector (A) containing a		
CC	DNA sequence (I) encoding a single-chain variable antibody fragment		
CC	(scFv). The products of the invention have antiviral, cytostatic and		
CC	immunostimulant activity and can be used in gene therapy, immunization		
CC	and diagnosis particularly of T cell-associated diseases, specifically		
CC	acquired immune deficiency syndrome (AIDS), severe combined immune		
CC	deficiency (SCID) or T cell lymphoma. (A) target T cells, independently		
CC	of the CD4 receptor, with high selectivity, 4-5 fold selectivity over		
CC	human B cells, and 1000 fold selectivity over other human cells. A vector		
CC	designated 7A5 encodes a 329 amino acid single-chain variable antibody		
CC	fragment, fully defined in the specification. It was used to transform		
CC	D17 (canine osteosarcoma cells susceptible to spleen necrosis virus		
CC	(SNV)) cells. C8166 (human T lymphocyte) cells, and HeLa (human cervical		
CC	carcinoma) cells. After 48 hours, the cells were stained with X-gal to		
CC	determine transformation. The viral titer (infectious units/ml) was over		
CC	1 million for D17, 1 million for C8166 but less than 100 for HeLa,		
CC	showing the high selectivity for human T cells. This sequence encodes the		
CC	SNV-env leader/human 7B4-scFv fusion construct used in the construction		
CC	of novel cell targeting vectors described in the invention. (Updated on		
CC	11-SEP-2003 to standardise OS field)		
XX			
SQ	Sequence 946 BP; 199 A; 249 C; 276 G; 222 T; 0 U; 0 Other;		
	Query Match 61.1%; Score 629.2; DB 5; Length 946;		
	Best Local Similarity 80.2%; Pred. No. 3.5e-148;		
	Matches 768; Conservative 0; Mismatches 178; Indels 12; Gaps 2		
Oy	44 ATGACCTGTCTCACCAACTCCGATCCGCTGAGGGTAAAGTTGACCAGCGCAGAAAATC 103		
Db	1 ATGACCTGTCTCACCAACTCCGATCCGCTGAGGGTAAAGTTGACCAGCGCAGAAAATC 60		
Oy	104 CTAATTCTCCTTGTCGGCTTGGTGGGGTTGGGACCATGCCGAGTTTCGACTGCCCGA 163		
Db	61 CTAATTCTCCTTGTCGGCTTGGTGGGGTTGGGACCATGCCGAGTTTCGACTGCCCGA 120		
Oy	164 CGGCCACAGCCGGCCATGGCCGAGGTCGAAGCTCAAGCTGCAGCAGTCAAGGGCTGAGCTGGTGGG 223		
Db	121 CGGCCACAGCCGGCCATGGCCGAGGTCGAAGCTCAAGCTGCAGCAGTCAAGGGCTGAGCTGGTGGG 180		
Oy	224 CCTGGGGTCTCAGTGAAGATTTCCTGCAAGGGTCTTGGCTACACATTCACTGATTATGGT 283		
Db	181 CCTGGAGCTTCAGTGAAGCTGTCTCTGCAAGACTTCTGGCTTCTCCTTACCAGCTACTTGG 240		
Oy	284 ATGAGCTGGGTGAACACAGATCATGCAAGAGTCTTAGAGTGGATTGGACTTATTAGTACT 343		
Db	241 ATGAATCGGGTGAAGCTGAGGCCCTGGACAAGGCCCTTGAGTGGATTGGCATGATTTCATCT 300		
Oy	344 TACTATGTGTGATCTCTAGTTTACAAACAGAGGTTTCAAGGGCAGGCCACAAATGACTGTAGAC 403		
Db	301 TCCGNATGTGAAC TAGTTTTAACTCAGAGGTTTCAAGGACAGGCCACACTGACTGTAGAC 360		
Oy	404 AAATCTCTCAAACACAGCCCTATTTTGGAAC TTGCCAGACTGACATCTTGAGGATTTCTGCCATT 463		

CC (VH) and light (VL) chain variable regions of antibody 8860 joined by an
CC artificial, flexible linker peptide; Escherichia coli alkaline
CC phosphatase; and a C-terminal 6His affinity tail. The DNA was used in the
CC construction of a miniantibody construct (see AAF30730), which was used
CC as negative control in determination of Factor VIII (FVIII)-like activity
CC of a 198/B1 miniantibody. 198/B1 is an example of anti-human Factor IX
CC (FIX)/activated Factor IX (FIXa) antibodies of the invention. Anti-
CC FIX/FIXa antibodies and their derivatives have FVIIIa cofactor or FIXa
CC activating activity. Administration leads to an increase in the
CC procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors.
CC This allows for rapid blood coagulation even in the absence of FVIII or
CC FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
CC derivatives are used in a claimed pharmaceutical composition for treating
CC patients with blood coagulation disorders, especially haemophilia A and
CC haemorrhagic diathesis. The scFv-alkaline phosphatase was expressed in E.
CC coli. It exhibited no FVIII-like activity

XX
SQ Sequence 2190 BP; 549 A; 579 C; 606 G; 456 T; 0 U; 0 Other;

Query Match 52.2%; Score 538; DB 4; Length 2190;
Best Local Similarity 80.3%; Pred. No. 3.9e-125;
Matches 647; Conservative 0; Mismatches 150; Indels 9; Gaps 1;

QY 137 ACCACTGCCGAAGTTTCGACTGCCGAGCGCCGAGCGCCCATGCCGAGGTCAAAGCTG 196
DB 19 ACGGACGCGCTGGATTGTTTACTCGCGGCCGAGCGGCCATGCCGAGGTTCAGCTT 78
QY 197 CAGCAGTCAAGGGCTGAGCTGGTGAGCGCTGGGGTCTCAGTGAAGATTTCCTGCAAGGGT 256
DB 79 CAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTCAGTGAAGATTTCCTGCAAGGT 138
QY 257 TCTGGCTCACATTCACTGATTGATGATGATGATGATGATGATGATGATGATGATGAT 316
DB 139 TCTGGCTACGATTCAGTACCTTGGATGAATCGGGTGAAGCAGAGGCTGGACAGGT 198
QY 317 CTAGAGTGGATTGCACTTATTAGTACTTACTATGTTGATCTTACTATCAACACAGAGTTT 376
DB 199 CTGAGTGGATTGACGGATTATCTCTGGAAATGGAGATACTTAACATACATGGGAAGTT 258
QY 377 AAGGGCAAGGCCCAATAGTCTAGAGAAATCTTCCAAACAGACCTATTGGAAGTTGCC 436
DB 259 AAGGGCAAGGCCCACTAGCTGAGACAAATCTCCAGCAGACCTACATGACGCTCAGC 318
QY 437 AGACTGACATCTGAGGATTCGCCATTATTATTGTCAGATCGGATGGTAATTACGGG 496
DB 319 AGCCTGACCTCTGTGACTCTGGGCTATTCTTGTGCA-----GATGGTAACGTA 369
QY 497 TATTACTATGCTTTGGACTACTGGGCGCAAGGCACTACGCTACCGTCTCCTCAGGTGGA 556
DB 370 TATTACTATGCTATGACTACTGGGCTCAAGNACCTCAGTACCGTCTCCTCAGGTGGA 429
QY 557 GCGGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGCTCACTCAGTCT 616
DB 430 GCGGGTTCAGGTGGCGCGCTCTGGCGGTGGCGGATCGCAATTGTTCTCACCAGTCT 489
QY 617 CCATCTCTCTTGGCTGTCTCTAGGGCAGAGGGCCACCATATCTTCGAGAGCCAGTGA 676
DB 490 CTGCTCTCTTACGCTGATCTCTCTGGGGCAGAGGGCCACCATCTCATGAGGGCCAGCAA 549
QY 677 AGTGTGTAGTATTATGGCGATAGTTTATGCACTGCTATCAGCAGAAACACAGGACAGCA 736
DB 550 AGTGTGAGTACATCTGGCTATAGTTATATGCACTGGTACCAACAGAAACACAGGACAGCA 609
QY 737 CCCAAATCTCTCATCTATCGTCATCCAACTAGAAATCTGGAGTCCCTGCCAGGTTCACT 796
DB 610 CCCAAATCTCTCATCTATCTTGATCCAACTAGAAATCTGGGTCCTGCCAGGTTCACT 669
QY 797 GGCAGTGGGTCTGAGTCAGACTTCACTCAATCGATCGTCTGTGAGGAAGATGATGCT 856
DB 670 GGCAGTGGGTCTGGGACAGACTTCACTTCAATCCATCATCTCTGTGAGGAGGAGTGTCT 729
QY 857 GCAGTGTATTACTGTCTGCAAGTATGGAAGATCCGTACACGCTTCGAGGGGGACCAAG 916

Db 730 GCAACCTATTACTGTCTCAGCACAGTAGGAGCTTCTCTCGAGCGTTCTGGTGGAGGCCAAG 789
QY 917 CTGGAATAAAGCGCGCGCGCGCATC 942
DB 790 CTGGAATCAAGCGCGCGCGCGCAGC 815
RESULT 7
AAF30734
ID AAF30734 standard; DNA; 876 BP.
XX
AC AAF30734;
DT 21-JUN-2001 (first entry)
XX
DE DNA encoding antibody 8860 scFv with c-myc-tag.
XX
KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag;
KW ds.
XX
OS Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..876
FT sig_peptide /*tag= a
FT /*tag= b
FT mat_peptide 67..873
FT /*tag= c
XX
PN WO200119992-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-EP008936.
XX
PR 14-SEP-1999; 99AT-00001576.
XX
PA (BAXT) BAXTER AG.
XX
PI Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX
XX WPI; 2001-290358/30.
XX P-PSDB; AAB20443.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 18; Fig 35; 138pp; English.
XX
XX The present sequence is that of DNA encoding a fusion protein (see
XX AAB20443) comprising (from the N-terminal end): a PelB leader sequence; a
XX single chain Fv (scFv) derivative of antibody 8860 comprising the heavy
XX (VH) and light (VL) chain variable regions of 8860 joined by an
XX artificial, flexible linker peptide; a Myc-tag and a C-terminal 6His
XX affinity tail. The fusion protein was expressed in Escherichia coli from
XX vector pMyChis6. The construct was used as a negative control to
XX determine the Factor VIII (FVIII)-like activity of a 198/B1 antibody scFv
XX fragment (see AAB20442) also expressed from pMyChis6. 198/B1 (clone AB2)
XX is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
XX antibodies of the invention. Anti-FIX/FIXa antibodies and their
XX derivatives, including scFv fragments, have FVIIIa cofactor activity or
XX FIXa activating activity. Administration leads to an increase in the
XX procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors.
XX This allows for rapid blood coagulation even in the absence of FVIII or
XX FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
XX derivatives are used in a claimed pharmaceutical composition for treating

CC patients with blood coagulation disorders, especially haemophilia A and
XX haemorrhagic diathesis
SQ Sequence 876 BP; 211 A; 233 C; 239 G; 193 T; 0 U; 0 Other;

Query Match 52.2%; Score 537.6; DB 4; Length 876;
Best Local Similarity 80.3%; Pred. No. 3.8e-125;
Matches 646; Conservative 0; Mismatches 149; Indels 9; Gaps 1;

QY 137 ACCACTGCCGAGTTTCGACTGCCCGAGCGGCCCGCCCATGCGCGAGGTCAAGCTG 196
DB 19 ACGGCAGCCGCTGGATTGTTATTACTCGCGGCCCGCCCATGCGCGAGGTTCAGCTT 78

QY 197 CAGCAGTCAGGGCTCAGCTGGTGAGCCCTCGGGCTCTCAGTGAAGATTTCCTCAAGGCT 256
DB 79 CAGCAGTCGACCTGAGCTGGTGAGCCCGGGGCTCAGTGAAGATTTCCTGCAAGCT 138

QY 257 TCTGGCTACACATTCATCTAGTATGATGAGCTGGGTGAACAGAGTCATGCAAGAGT 316
DB 139 TCTGGCTACGATTCAGTAGCTCTTGGATGAACCTGGGTGAAGCAGAGGCTGGACAGGT 198

QY 317 CTAGAGTGGATTGGACTTATTAGTACTTACTATGGTGATCCTAGTTTACAACAGAGTTTC 376
DB 199 CTTGAGTGGATTGGACGGATTTATCTCGGAATGGAGATACTAACTACAATGGGAAGTTTC 258

QY 377 AAGGGCAAGGCCACAATGACTGTAGACAAATCTCCAAACACAGCCTATTTCGAACTTGCC 436
DB 259 AAGGGCAAGGCCACATGACTGCAGACAAATCTCCAGCACAGCCTACATGAGCTCAGC 318

QY 437 AGACTGACATCTGAGGATCTGCATTTATTATTGTGCAAGATCGGATGGTAAATTACGGG 496
DB 319 AGCTGACCTCTGTGACTCTGGGCTCTATTCTGTGCA-----GATGTAACGTA 369

QY 497 TATTACTATGCTTTGGACTACTGGGGCCAGGCACCTACGGTCAACCGTCTCCTCAGTGGA 556
DB 370 TATTACTATGCTATGACTACTGGGGTCAAGGAACCTCAGTCAACCGTCTCCTCAGTGGA 429

QY 557 GGCGGTTACAGGCGAGGTGGCTCTGGCGGTGGGGATCGGATACCGTCAACCGTCTCCTCAGTGCT 616
DB 430 GGCGGTTACAGTGGCGCGCTCTGGCGGTGGGGATCGCAATTGTTCTCACCAGTCT 489

QY 617 CCATCTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACCATATCTCTGACAGCCAGTGAA 676
DB 490 CTTGCTCTCTTAGCTGTATCTCTGGGCGAGAGGCCACCATCTCATGCGAGGCCAGCAA 549

QY 677 AGTGTGATAGTTATGGCGATGTTTATGCACTGGTATCAGAGAAACAGGACAGCCA 736
DB 550 AGTGTGATGATCTGGCTATAGTTATATGCACTGGTATCAACAGAAACAGGACAGCCA 609

QY 737 CCCAAACTCTCATCTATCTGTCATCCAACTAGATCTGGAGTCCCTGCGAGTTTCAGT 796
DB 610 CCCAAACTCTCATCTATCTTGATCCAACTAGATCTGGGTCCTGCGAGTTTCAGT 669

QY 797 GGCACTGGGTCTGAGTCAGACTTCATCTCAACATGATCTCTGTGAGGAAGATGCT 856
DB 670 GGCACTGGGTCTGGGACAGACTTCACCCCTCAACATCTCTGTGAGGAGGAGTGTCT 729

QY 857 GCAGTGTATTACTGTCTGCAAGTATGAGATCCGTACACGTTTCGAGGGGGACCAAG 916
DB 730 GCAACCTATTACTGTGAGCACATAGGAGCTTCTCTCGGACGTTTCGTTGAGGACCAAG 789

QY 917 CTGGAATAAAACGGGCGCGCA 940
DB 790 CTGGAATAAAACGGGCGCGCA 813

RESULT 8
AAF30730
ID AAF30730 standard; DNA; 969 BP.
XX
AC AAF30730;
XX DT 21-JUN-2001 (first entry)

Query Match 52.2%; Score 537.4; DB 4; Length 969;
Best Local Similarity 80.2%; Pred. No. 4.4e-125;
Matches 647; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

QY 137 ACCACTGCCGAGTTTCGACTGCCCGAGCGGCCCGCCCATGCGCGAGGTCAAGCTG 196
DB 19 ACGGCAGCCGCTGGATTGTTATTACTCGCGGCCCGCCCATGCGCGAGGTTCAGCTT 78

QY 197 CAGCAGTCAGGGCTGAGCTGTGAGGCTCTGGGCTCTCAGTGAAGATTTCCTCAAGGCT 256

XX Antibody 8860 bivalent miniantibody DNA.
DE Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW bivalent antibody; p8860-Zip#1.2; ds.
XX Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
FH Key Location/Qualifiers
CDS 1..969
FT /*tag= a
FT sig_peptide 1..66
FT /*tag= b
FT /*note= "PelB leader sequence"
FT mat_peptide 67..966
FT /*tag= c
XX WO200119992-A2.
PN 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP008936.
XX
XX 14-SEP-1999; 99AT-00001576.
XX (BAXT) BAXTER AG.
XX
PI Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX WPI; 2001-290358/30.
DR P-PSDB; AAB20440.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 16; Fig 30; 138pp; English.
XX
XX The present sequence is that of the coding region of plasmid p8860-
CC Zip#1.2 encoding a bivalent miniantibody (see AAB20440) comprising the
CC single chain Fv (scFv) fragment of antibody 8860 fused to an amphipathic
CC helical structure. The plasmid was obtained by inserting 8860 scFv DNA
CC into vector pZipl. The construct was used as negative control in
CC examination of the Factor VIII (FVIII)-like activity of an antibody
CC 193/B1 miniantibody (see AAB20438). 193/B1 is an example of anti-human
CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
CC Anti-FIX/FIXa antibodies and their derivatives have FVIIIa cofactor
CC activity or FIXa activating activity. Administration leads to an increase
CC in the procoagulant activity of FIXa, even in the presence of FVIIIa
CC inhibitors. This allows for rapid blood coagulation even in the absence
CC of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The
CC antibodies and derivatives are used in a claimed pharmaceutical
CC composition for treating patients with blood coagulation disorders,
CC especially haemophilia A and haemorrhagic diathesis. The present bivalent
CC miniantibody exhibited no FVIII-like activity
XX
SQ Sequence 969 BP; 233 A; 257 C; 264 G; 215 T; 0 U; 0 Other;

Db 79 CAGCAGTCTGGACCTGAGCTGGTGAAGCCGGGCGCTCAGTGAAGATTTCTCTGCAAGCT 138
Qy 257 TCTGGCTACACATTCACATGATTATGGTATGAGCTGGGTGAACAGAGTCAATGCAAGAT 316
Db 139 TCTGGCTACACATTCACATGATTATGGTATGAGCTGGGTGAACAGAGTCAATGCAAGAT 198
Qy 317 CTAGAGTGGATTGAGCTTATTTAGTCTTACTATGTTGATCTCTAGTATCAACACAGAGTTC 376
Db 199 CTTGAGTGGATTGAGCGGATTTATCTGGAAATGGAGATTAATACTAATGGAAGTTC 258
Qy 377 AAGGGCAAGGCCAACAATGAGCTAGACAAATCTCCAAACAGCCTATTTTGGAACTTGGC 436
Db 259 AAGGGCAAGGCCAACAATGAGCTAGACAAATCTCCAAACAGCCTATTCAGCTCAGC 318
Qy 437 AGACTGACATCTGAGGATCTGCCATTTATTTGTCAGAGATCGGATGATTAATACGG 496
Db 319 AGCTGACCTCTGGGACTCTGGGCTCTGCGTCTTTCTGTGCA-----GATGGTAACGTA 369
Qy 497 TATTACTATCTTTGGACTACTGGGGCAAGGCACTACGGTCAACCGTCTCTCAGGTGGA 556
Db 370 TATTACTATCTGAGTACTGGGGTCAAGGAACCTCAGTCAACCGTCTCTCAGGTGGA 429
Qy 557 GCGGTTTCAGGCGGAGTGGCTCTGGCGGTGGCGGATCGGATATCGAGTCACTCAGTCT 616
Db 430 GCGGTTTCAGGCGGCGCTCTGGCGGTGGCGGATCGGATATCGGATATCGGATATCGG 489
Qy 617 CCATCTCTTTGGTGTCTCTAGGGCAGAGGCGCAACATATCTCGCAGAGCGAGTGA 676
Db 490 CCGTCTCTCTTCTAGCTGTATCTCTGGGGCAGAGGCGCAACATATCTCGCAGAGCGAG 549
Qy 677 AGTGTGATGATGATGCGGATGTTTATGCACTGGTATCAGCAGAAACAGGACAGCCA 736
Db 550 AGTGTGATGATGATGCGGATGTTTATGCACTGGTATCAGCAGAAACAGGACAGCCA 609
Qy 737 CCCAAATCTCTATCTATCTGATCAACCTAGAACTCTGGAGTCCCTGCGAGGTTTCAGT 796
Db 610 CCCAAATCTCTATCTATCTGATCAACCTAGAACTCTGGAGTCCCTGCGAGGTTTCAGT 669
Qy 797 GGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCTCTGAGGAGGAATGATGCT 856
Db 670 GGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCTCTGAGGAGGAATGATGCT 729
Qy 857 GCAGTGTATTACTGTCTGCAAGTATGGAAGATCCGTACAGTTCGGAGGGGGGACCAAG 916
Db 730 GCAACCTATTACTGTCTGACAGCAGTAGGAGCTTCTCTCGGACGTTCTCGGTGAGGACCAAG 789
Qy 917 CTGCAATAAAGCGGGCGCGCATCG 943
Db 790 CTGCAATAAAGCGGGCGCGCACCG 816

RESULT 9

ADL07528
ID ADL07528 standard; DNA; 744 BP.
XX
AC ADL07528;
XX
DT 06-MAY-2004 (first entry)
XX
DE P. pastoris ScFv-43 DNA.
XX
KW scFv-LDP; ScFv-43; type IV collagenase; single-chain Fv fragment;
KW Lidamycin agon protein; LDP; methanol nourishing yeast; vascularisation;
KW tumour; invasive metastasis; antibody; ds.
XX
OS Pichia pastoris.
XX
PN CN1403577-A.
XX
PD 19-MAR-2003.
XX
PF 06-SEP-2001; 2001CN-00131299.
XX

PR 06-SEP-2001; 2001CN-00131299.
XX (MEDI-) INST MEDICINAL BIOTECHNOLOGY CHINESE ACA.
PA Zhen Y, Tang Y;
XX WPI; 2003-505669/48.
XX Fusion protein of type IV collagenase resistant single chain antibody and
PT Lidamycin agon protein.
XX Disclosure; SEQ ID NO 1; 18pp; Chinese.
XX The invention relates to the construction of one small fusion protein
CC scFv-LDP by DNA molecular recombination technology and gene engineering
CC technology to constitute the fusion gene of type IV collagenase resisting
CC single-chain Fv fragment, (scFv) gene and Lidamycin agon protein (LDP).
CC The fusion gene is expressed in methanol nourishing yeast Pichia pastoris
CC and the expressed fusion protein has its binding capacity for antigen
CC type IV collagenase maintained and has inhibits vascularisation of chick
CC embryo allantois membrane. The fusion protein may also function as a
CC double-function small monoclonal antibody guide medicine with the
CC activity of killing tumour cells and of inhibiting invasive metastasis.
CC The present sequence is the Pichia pastoris ScFv-43 DNA.
XX Sequence 744 BP; 179 A; 175 C; 216 G; 174 T; 0 U; 0 Other;

Query Match 52.1%; Score 536.8; DB 10; Length 744;
Best Local Similarity 83.2%; Pred. No. 5.8e-125;
Matches 626; Conservative 0; Mismatches 117; Indels 9; Gaps 1;

Qy 179 ATGCGCGAGTCAAGCTGACAGCTCAGGGGCTGAGCTGGTGGCTGAGCTGGTGGTCAAGT 238
Db 1 ATGCGCGAGTCAAGCTGACAGCTCAGGGGCTGAGCTGGTGGTGGTCAAGTGGGCTTCAGTG 60
Qy 239 AAGATTTCTGCAAGGTTCTGGCTACACATTCACATTCATGATGATGATGATGATGATGAT 298
Db 61 AAGTTGTTCTGCAAGGTTCTGGCTACACATTCACATTCATGATGATGATGATGATGATGATG 120
Qy 299 CAGAGTCATGCAAGAGTCTAGAGTGGATGGATCTTATAGTACTTATAGTACTTATAGTACT 358
Db 121 CAGACGCTGCAACAGGACTTGAAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 180
Qy 359 AGTTACACACAGAGTTCAGGGCAGGCGCACATGACTGTAGACAAATCTCTCAACACA 418
Db 181 GAATACAAATGAGAAGTTCAAGGGCAGGCGCACATGAGTGTAGACAAATCTCTCAACACA 240
Qy 419 GCCTATTTGGAACTTCCAGACTGACATCTGAGGATTTCTGCCATTTATTTATTTGCAAGA 478
Db 241 GCCTATATGAGCTCACTAGGCTGACATCTGAGACTCTGCTGTCTATTTCTGTGCTAGA 300
Qy 479 TCGGATGGTAAATTAACGGGTATTAATGCTTTGGACTTCTGGGCGCAAGGCACCTACGGTC 538
Db 301 GGGGACTACTATAGGCGCTA-----CTTTGACTTTGTGGGCGCAAGGCACCGGTC 351
Qy 539 ACCGTCTCTCAGGTGAGCGGTTTCAAGCGAGAGTGGCTCTGCGGTGCGGATCGGAT 598
Db 352 ACCGTCTCTCAGGTGAGCGGTTTCAAGCGAGAGTGGCTCTGCGGTGCGGATCGGATCGGAC 411
Qy 599 ATCGAGCTCACTCAGTCTCCATCTTCTTGGCTGTGTCTTAGGGCAGAGGGCCACCATA 658
Db 412 ATCGAGCTCACTCAGTCTCCAGCTTCTTTGGCTGTGTCTTAGGGCAGAGGGCCACCATA 471
Qy 659 TCCTGCGAGGCCAGTGAAGTGTGTAGTATGGCGATAGTATTTATGCACTGGTATCAG 718
Db 472 TCCTGCGAGGCCAGTGAAGTGTGTAGTATGGCGATAGTATTTATGCACTGGTATCAG 531
Qy 719 CAGAAACAGGACAGCCACCCAAATCTCTCATCTATGTCGATCCCAACCTAGAAATCTGGA 778
Db 532 CAGAAACAGGACAGCCACCCAAATCTCTCATCTATCTTCAACCAACCTAGAAATCTGGG 591
Qy 779 GTCCCTGCCAGGTTTCAGTGGCAGTGGTCTGAGTCAGACTTCACTCTCACCATCGATCCT 838

Db 592 GTCCCTGCCAGGTTTCAGTGGCTAGTGGCTTAGGACAAATTCACCTCACCATTGATCCT 651
QY 839 GTGGAGGAGATGATGCTGCAGTGTATTACTGCTGCAAGTATGGAAGATCCGTACACG 898
Db 652 GTGGAGGCTGATGATGCTGCACCTATTACTGTGACGAAATAATGAGGATCCGTACACG 711
QY 899 TTTCGAGGGGGGACCAAGCTGGAAATAAAACG 930
Db 712 TTTCGAGGGGGCACCAAGCTGGAAATCAAACG 743

RESULT 10
AAA60982
ID AAA60982 standard; DNA; 1094 BP.
XX
AC AAA60982;
XX
XX 08-NOV-2000 (first entry)
DE
DT Antibody nucleotide sequence.
XX
XX Lida-protein; LDP; Lida-chromophore; LDC; antibody; lidamycin;
KW antibiotic; anticancer; tumour; cancer; ds.
XX
OS Synthetic.
XX
XX CN1251840-A.
PN
XX 03-MAY-2000.
PD
XX 13-OCT-1999; 99CN-00121668.
PF
XX 13-OCT-1999; 99CN-00121668.
PR
XX (MEDI-) INST MEDICINAL BIOTECHNOLOGY CHINESE ACA.
PA
XX
PI Zhen Y, Li S, Jiang M;
DR WPI; 2000-432052/38.
XX
XX Constitutive fusion protein of ridamycin as anticancer antibiotic and
PT single-chain antibody.
XX
XX Disclosure; Page 2-3; 18pp; Chinese.
XX
XX The present invention describes a fusion protein, designated Lidamycin,
CC composed of Lida-protein (LDP) and Lida-chromophore (LDC), which acts as
CC an anticancer antibiotic and single-chain antibody. LDP and LDC are
CC joined via non-covalent bonds and can be splitted and recombined. A
CC single-chain antibody scFv can specifically join with IV-type collagenase
CC and can suppress its activity and in order to increase the permeability
CC of medicine to capillary tubes and the penetrability to real tumour, DNA
CC recombination and molecular recombination are used to prepare new-type
CC constitutive fusion protein LDM-Fv of anticancer targeting medicine
CC Lidamycin and single-chain antibody. Its molecular weight is about 37KDa.
CC It has the activity to inhibit IV-type collagenase and strong intrusion-
CC resistance kill action to cancer cells. It may be an ideal clinic
CC medicine. The present sequence represents an antibody nucleotide sequence
CC given in the exemplification of the present invention
XX
XX Sequence 1094 BP; 230 A; 312 C; 325 G; 227 T; 0 U; 0 Other;

Query Match 51.1%; Score 526.2; DB 3; Length 1094;
Best Local Similarity 82.8%; Pred. No. 3e-122;
Matches 622; Conservative 0; Mismatches 108; Indels 21; Gaps 1;
QY 179 ATGCCGAGGTCAAGCTGCAGCAGTCAAGGGGCTGAGCTGGTGGGCTGGGGTCTCAGTG 238
Db 1 ATGCCGAGGTCAAGCTGCAGCAGTCTGGACCTGAACCTGGTGAAGCTGGGGCTTTAGTG 60
QY 239 AAGATTCTCTGAAGGTTCTGGCTACACATTCACTGATTATGTTATGAGCTGGGTGAA 298
Db 61 AAAATATCTGCAAGGCTTCTGGTTACACCTTCACAGACTACGATATAAACTGGGTGAAG 120

QY 299 CAGAGTCATGCAAAAGAGTCTAGAGTGGATTGGACTTATTAGTACTTACTATGGTATCCT 358
Db 121 CAGAGGCTGGACAGGACTTGGTGGATTGGATGGATTATCTCTGGAGATGGTAGTGCT 180
QY 359 AGTTACAACACGAGGTTCAAGGGCAAGGCCAACATGACTGTAGACAAATCTCTCCAAACA 418
Db 181 AAGTACAATGAGAAAGTTCAAGGGCAAGGCCAACATGACTGCAGACAAATCTCTCCAGACA 240
QY 419 GCCTATTGGAACTTGCAGACTGCATCATCTGAGGATTCTGCCATTTATTATTGTGCAAGA 478
Db 241 GCCTACATGACGTCAGCAGCCTGACTTCTGAGAACTCTGCAGTCTTATTCTGTGCAAGA 300
QY 479 TCGGATGGTAATTAACGGGTATTACTATGCTTTTGGACTACTGGGGCCCAAGGCACCTACGGTC 538
Db 301 GGG-----CATAACTTTGACTACTGGGGCCCAAGGCACCGGTC 339
QY 539 ACCGTCCTCCTCAGGTGGAGCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGAT 598
Db 340 ACCGTCCTCCTCAGGTGGAGCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGAC 399
QY 599 ATCGAGCTCAGTCAGTCTCCATCTTTTGGCTGTGTCTTAGGGCAGAGGGCCACATA 658
Db 400 ATCGAGCTCAGTCAGTCTCCAGCTTCTTTGGCTGTGTCTTAGGGCAGAGGGCCACATA 459
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Db 460 TCTCTGAGAGCCAGTGAAAGTGTGATAGTTATGGCGATAGTTTATGCTGGTACCAG 519
QY 719 CAGAAACAGGACAGCCACCCAACTCTCATCTATCGTGCATCCAACTAGAAATCTGGA 778
Db 520 CAGAAACAGGACAGCCACCCAACTCTCATCTATCTTTGCAACCAACTTAGGATCTGG 579
QY 779 GTCCCTGCCAGGTTCAAGTGGCGAGTGGTCTGAGTCAGACTTCACTCTCACCATCGATCCT 838
Db 580 GTCCCTGCCAGGTTCAATGGCAGTGGGTTTAGGACAAACTTCACCCCTCACCATCGATCCT 639
QY 839 GTGGAGGAAGATGATGCTGCAGTGTATTACTGTCTGCAAGATATGGAAGATCCGTACACG 898
Db 640 GTGGGGGCTGATGATGCTGCAACCTATTACTGTGCAAAATAATGAGGATCCGTACACG 699
QY 899 TTTCGAGGGGGGACCAAGCTGGAATAAAAC 929
Db 700 TTTCGAGGGGGGACCAAGCTGGAATAAAAC 730

RESULT 11
AAZ44206
ID AAZ44206 standard; DNA; 925 BP.
XX
AC AAZ44206;
XX
DT 31-MAR-2000 (first entry)
XX
DE Murine derived DNA fragment #4.
XX
XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine; ds.
XX
OS Mus sp.
XX
XX WO9961629-A1.
XX
XX 02-DEC-1999.
PD
XX 24-MAY-1999; 99WO-JP002711.
PF
XX 25-MAY-1998; 98JP-00159957.
PR
XX 26-MAY-1998; 98JP-00163023.
PR
XX (ASAH) ASAH KASEI KOGYO KK.
PA (ASAH) ASAH MEDICAL CO LTD.

```
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX WPI: 2000-086720/07.
XX P-PSDB; AAY51142.
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells.
XX Claim 22; Page 82-84; 11pp; Japanese.
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for the
XX collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal compositions
XX for the treatment of HIV infection and autoimmune diseases. This sequence
XX encodes a murine derived protein fragment which is used to illustrate the
XX method of the invention
XX
XX Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 U; 0 Other;
XX
XX Query Match 50.7%; Score 522.6; DB 3; Length 925;
XX Best Local Similarity 79.3%; Pred. No. 2.3e-121;
XX Matches 637; Conservative 0; Mismatches 154; Indels 12; Gaps 1;
XX
XX QY 136 GACCACCTGCGAAGTTTCGACTCCCGAGCGGCCGAGCCGATGCGGAGGTCGAAGCT 195
XX DB 18 GACCGCTGCTGGTCTGCTGCTCCGCGGCCGAGCGGCCATGSCCCAGGTTCAAGCT 77
XX
XX QY 196 GCAGCAGTCAAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 255
XX DB 78 GCAGCAGTCAAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 137
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XX QY 256 TTCTGGCTACACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTC 315
XX DB 138 TTCTGGATACACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTC 197
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XX QY 316 TCTAGAGTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGG 375
XX DB 198 CTTGAGTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGGATTGG 257
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XX QY 376 CAAAGGCAAGGCCCAACATGACTGTGACAAATCTCTCAACACAGAGCTATTTTGAACCTTGC 435
XX DB 258 CAAAGGCAAGGCCCAACATGACTGTGACAAATCTCTCAACACAGAGCTATTTTGAACCTTGC 317
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XX QY 436 CAGACTGACATCTGAGGATTTCTGCCATTTATTTATTTGCAAGATCGGATGTAATTACGG 495
XX DB 318 CAGCCTGACATCTGAGGATTTCTGCCATTTATTTATTTGCAAGATCGGATGTAATTACGG 365
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XX QY 496 GTATTACTATGCTTTGGACTACTGGGGCCCAAGGCACTACGGTCCACCGTCTCTCTCAGGTGG 555
XX DB 366 AACTGGGACGGGTTTGGCTTACTTGGGGCCGAGGACTCTGGTCACTGTCTCTCAGGTGG 425
XX
XX QY 556 AGCGGTTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATCGGATCGGATCGGATCGGATCG 615
XX DB 426 AGCGGTTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATCGGATCGGATCGGATCGGATCG 485
XX
XX QY 616 TCCATCTTTTGGCTGTCTCTAGGCGAGGGCCACATATCTCTGAGAGCCAGTGA 675
XX DB 486 TCCAGCTTTTGGCTGTCTCTAGGCGAGGGCCACATATCTCTGAGAGCCAGTGA 545
XX
XX QY 676 AAGTGTGTAGTATGGGATAGTTTATGCACTGGTATCAGCAAGAAACACAGGACAGCC 735
XX DB 546 AAGTGTGTATGATGGTATAGTTTATGCACTGGTATCAGCAAGAAACACAGGACAGCC 605
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XX QY 736 ACCAAACTCTCATCTATCGTGATCCCAACTAGAAATCTGGAGTCCCTGCGCAGGTTTCAAG 795
XX DB 606 ACCAAACTCTCATCTATCGTGATCCCAACTAGAAATCTGGAGTCCCTGCGCAGGTTTCAAG 665
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XX
XX Db 726 TGCACACTATTACTGTCTGACCAAGATAGTAGGATCTCTCCGACGTTCTGGTGGAGGACCA 785
XX
XX QY 916 GCTGGAATATAAAGCGGCGCGCG 938
XX
XX Db 786 GCTGGAATATAAAGCGGCGCGCG 808
XX
XX RESULT 12
XX AAZ58664
XX ID AAZ58664 standard; cDNA to mRNA; 925 BP.
XX AC AAZ58664;
XX DT 17-APR-2000 (first entry)
XX DE Antibody 4H5 L chain encoding nucleotide sequence.
XX CD4 antigen; anti-human; antibody; 4H5; drug; ds.
XX Mus sp.
XX JPL1332563-A.
XX 07-DEC-1999.
XX 26-MAY-1998; 98JP-00163034.
XX 26-MAY-1998; 98JP-00163034.
XX (ASAH ) ASAH KASBI KOGYO KK.
XX WPI: 2000-091351/08.
XX P-PSDB; AAY59265.
XX An antibody and the nucleic acid coding the antibody.
XX Disclosure; Page 17-18; 25pp; Japanese.
XX The invention provides an antibody having affinity to CD4 antigen. The
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
XX application for drugs. It is highly safe in human dose. The present
XX sequence represents the antibody 4H5 L chain encoding nucleotide sequence
XX
XX Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 U; 0 Other;
XX
XX Query Match 50.7%; Score 522.6; DB 3; Length 925;
XX Best Local Similarity 79.3%; Pred. No. 2.3e-121;
XX Matches 637; Conservative 0; Mismatches 154; Indels 12; Gaps 1;
XX
XX QY 136 GACCACCTGCGAAGTTTCGACTCCCGAGCGGCCGAGCCGATGCGGAGGTCGAAGCT 195
XX DB 18 GACCGCTGCTGGTCTGCTGCTCCGCGGCCGAGCGGCCATGSCCCAGGTTCAAGCT 77
XX
XX QY 196 GCAGCAGTCAAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 255
XX DB 78 GCAGCAGTCAAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 137
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XX QY 256 TTCTGGCTACACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTC 315
XX DB 138 TTCTGGATACACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTC 197
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XX QY 436 CAGACTGACATCTGAGGATTTCTGCCATTTATTTATTTGCAAGATCGGATGTAATTACGG 495
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XX DB 366 AACTGGGACGGGTTTGGCTTACTTGGGGCCGAGGACTCTGGTCACTGTCTCTCAGGTGG 425
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XX DB 426 AGCGGTTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATCGGATCGGATCGGATCGGATCG 485
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XX DB 486 TCCAGCTTTTGGCTGTCTCTAGGCGAGGGCCACATATCTCTGAGAGCCAGTGA 545
XX
XX QY 676 AAGTGTGTAGTATGGGATAGTTTATGCACTGGTATCAGCAAGAAACACAGGACAGCC 735
XX DB 546 AAGTGTGTATGATGGTATAGTTTATGCACTGGTATCAGCAAGAAACACAGGACAGCC 605
XX
XX QY 736 ACCAAACTCTCATCTATCGTGATCCCAACTAGAAATCTGGAGTCCCTGCGCAGGTTTCAAG 795
XX DB 606 ACCAAACTCTCATCTATCGTGATCCCAACTAGAAATCTGGAGTCCCTGCGCAGGTTTCAAG 665
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XX QY 796 TGSCAGTGGTCTGAGTCAGACTTCACTCTCACCATCGATCTCTGTGGAGGAGATGATGC 855
XX
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 68479089

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	386.2	37.5	671	3 AF240168	Mus muscu
2	336.4	32.7	535	3 AF240170	Mus muscu
3	336.4	32.7	540	3 AF240167	Mus muscu
4	333.8	32.4	683	3 AF240172	Mus muscu
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6	313.2	30.4	1104	7 CK629846	AM2-AA002
7	311.2	30.2	601	5 BQ474958	carabus49
8	292.6	28.4	1339	7 CK629414	AM1-AA001
9	292.4	28.4	1419	7 CK629415	AM1-AA001
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11	282.4	27.4	407	2 AW988429	ug08d07.y
12	282.4	27.4	672	7 CK633068	AM3-AP001
13	282.4	27.4	672	7 CK633069	AM3-AP001
14	282.2	27.4	876	4 B1107286	602894285
15	277.4	26.9	327	4 BG148320	uu91c06.y
16	274.2	26.6	732	4 BG962768	602830291
17	271.4	26.3	565	2 BF801321	MRO-CI002
18	270.2	26.2	823	7 CK632348	AM0-AM000
19	269	26.1	738	4 BG965088	602829160
20	266.4	25.9	569	7 CK332703	H8210E01-
21	264.8	25.7	643	6 BY733441	BY733441
22	262.8	25.5	774	2 BF581989	602099444
23	262.2	25.5	544	5 BQ310337	MRO-BP450
24	258.4	25.1	922	2 BF584560	602098269

25	257	25.0	831	4 BG966589	602834422
26	253.6	24.6	490	4 B1050614	PM1-GN040
27	251.6	24.4	489	2 BF855922	PM2-FN021
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29	249	24.2	398	1 AA423447	ve80a03.i
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32	246.6	23.9	402	1 A1549800	ve80a03.y
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37	244.6	23.7	633	4 BG961755	602826375
38	243.2	23.6	442	5 BQ342972	PM0-NN022
39	243	23.6	311	3 AF240175	Mus muscu
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ALIGNMENTS

RESULT 1	AF240168	Mus musculus MRP5 mRNA, partial cds.	671 bp	linear	HTC 30-APR-2001
LOCUS	AF240168	AF240168.1	GI:13877288		
DEFINITION	AF240168	HTC.			
VERSION	AF240168.1	GI:13877288			
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 671)				
AUTHORS	Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H., Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.				
TITLE	Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice				
JOURNAL	World J. Gastroenterol. 6 (5), 709-717 (2000)				
PUBMED	11819679				
REFERENCE	2 (bases 1 to 671)				
AUTHORS	Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.				
TITLE	Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain				
JOURNAL	Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80 (2001)				
REFERENCE	3 (bases 1 to 671)				
AUTHORS	Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X. and Su,C.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China				
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CDS					

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Matches 506;   Conservative 0;   Mismatches 163;   Indels 12;   Gaps 1;
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QY 224  CTTGGGGTCTCAGTGAAGATTTCTCGAAGGGTTCTGGCTACACATTCAGTATGATGTT 283
DB 63   CTTGGAGAGACAGTCAGGATCTCTCGAAGGTTCTGGATATACCTTCACAACCTGCTGGA 122
QY 284  ATCAGCTGGGTGAACACAGAGTCATGCAAGAGTCTAGAGTGGATTGCACTTATTAGTACT 343
DB 123  ATCAGTGGGTGCAAAAGATGCCAGGAAGGGTTTGAAGTGGATTGGCTGGATAAACACC 182
QY 344  TACTATGGTGATCCTTAGTTACAAACACAGAGGTTCAAGGGCAAGGCCACAATGACTGTAGAC 403
DB 183  CACTCTGGAGTGCMAAGTATGCAGAAAGTTTCAAGGGAGCTTTGCCCTCTCTTTGGAA 242
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QY 464  TATTATTGTGCAAGATCGGATGCTAATACGGGTATTACTATGCTTTGGACTACTGGGC 523
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DB 411  AGTGGCGGATCGGACATCGTGCTCACCCAGTCTCCAGCTTCTTTGGCTGTGTCTTAGGG 470
QY 644  CAGAGGGCCACCATATCTCTCGACAGCCAGTGAAGTGTGATAGTTATGGCGATAGTTT 703
DB 471  CAGAGGGCCACCATCTCTCTCGACAGCCAGGAAAGTGTGATATATTGGCATTAGTTT 530
QY 704  ATGCACTGGTATCAGCAGAAACAGGACAGCCACCAAACTCCTCATCTATCGTGCATCC 763
DB 531  ATGAACTGGTTCAGCAGAAACAGGACAGCCACCAAACTCCTCATCTATGCTGCATCC 590
QY 764  AACCTAGATCTGGATCCCTCGCAGGTTTCAGTGGCAGTGGGTTCTAGTCAGACTTCACT 823
DB 591  AAGCAAGGATCCGGGGTCCCTCGAGGTTTACTGGCAAGTGGGTTCTGGGACAGATTTTCAGC 650
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DB 651  CTCAACATATATCCTATGGAG 671
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LOCUS      AF240170      535 bp      mRNA      linear      HTC 30-APR-2001
DEFINITION Mus musculus MRP7 mRNA.
ACCESSION  AF240170
VERSION    AF240170.1  GI:13877291
KEYWORDS   HTC.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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REFERENCE
AUTHORS      Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H.,
              Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.
TITLE        Mechanism of exogenous nucleic acids and their precursors improving
              the repair of intestinal epithelium after gamma-irradiation in mice
JOURNAL      World J. Gastroenterol. 6 (5), 709-717 (2000)
PUBMED       11819679
REFERENCE
AUTHORS      Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
TITLE        Cloning of mouse genes related to repairing of intestinal
              epithelium of the irradiated mice by treatment with the intestinal
              RNA of mice of the same strain
JOURNAL      Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80
              (2001)
REFERENCE
AUTHORS      Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.
              and Su,C.
TITLE        Direct Submission
JOURNAL      Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of
              Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang
              Le West Road, Xi'an 710032, China
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DB 534  GCGGCCCGCCGCTAGTGGCCGAGGTCAGCTCAGCTGCAGCTCAGGGCTGAGCTGGTGAGG 475
QY 224  CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTTCTGGCTACACATTCAGTATGATGTT 283
DB 474  CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTTCTGGCTACACATTCAGTATGATGTT 415
QY 284  ATGAGCTGGGTGAAACACAGAGTCATGCAAGAGTCTAGAGTGGATTGGACTTATTAGTACT 343
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QY 344  TACTATGTTGATCCTAGTTTACACACAGAGGTTTCAAGGGCAAGGCCACAATGACTGTAGAC 403
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QY 464  TATTATTGTGCAAGATCGGATGGTAATTACGGGTATTACTATGCTTTTGGACTACTCGGGC 523
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DB 177  CAAGGACCAACGGTCAACCGTCTCTCAGGTGGAGGGGTTTCAGGCGGAGTGGCTCTGGC 118
QY 584  GGTGGCGGATCGGA 597
DB 117  GGTGGCGGATCGGA 104
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RESULT 3
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LOCUS AF240167 540 bp mRNA linear HTC 30-APR-2001
DEFINITION Mus musculus MRP4 mRNA, complete cds.
ACCESSION AF240167
VERSION AF240167.1 GI:13877286
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 540)
AUTHORS Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H.,
Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.
TITLE Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice
JOURNAL World J. Gastroenterol. 6 (5), 709-717 (2000)
PUBMED 11819679
REFERENCE 2 (bases 1 to 540)
AUTHORS Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
TITLE Cloning of mouse genes related to repairing of intestinal
epithelium of the irradiated mice by treatment with the intestinal
RNA of mice of the same strain
JOURNAL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80
(2001)
REFERENCE 3 (bases 1 to 540)
AUTHORS Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.
and Su,C.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of
Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang
Le West Road, Xi'an 710032, China
LOCATION/Qualifiers
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CDS
Query Match 32.7%; Score 336.4; DB 3; Length 540;
Best Local Similarity 87.6%; Pred. No. 1.2e-83;
Matches 380; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 164 GCGGCCCGCCGCGCCATGCGCGAGGTCACGTCACAGTCAGTCAGGCGCTGAGCTGGTGGAGG 223
DB 9 GCGGCCCGCCGCGCCATGCGCGAGGTCACGTCACAGTCAGTCAGGCGCTGAGCTGGTGGAGG 68

QY 224 CTGCGGGTCTCAGTGAAGATTTCTCTCAAGGGTTCTGGCTACACATTCACATGATATGTT 283
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QY 284 ATGAGCTGGGTGAACAGAGCTATGCAAGAGTGCTCAGAGTGGATTCGACTTATTAAGTACT 343
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QY 584 GGTGGCGGATCGGA 597
Db 426 GGTGGCGGATCGGA 439

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LOCUS AF240172 683 bp mRNA linear HTC 30-APR-2001
DEFINITION Mus musculus MRP9 mRNA, partial cds.
ACCESSION AF240172
VERSION AF240172.1 GI:13877293
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 683)
AUTHORS Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H.,
Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.
TITLE Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice
JOURNAL World J. Gastroenterol. 6 (5), 709-717 (2000)
PUBMED 11819679
REFERENCE 2 (bases 1 to 683)
AUTHORS Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
TITLE Cloning of mouse genes related to repairing of intestinal
epithelium of the irradiated mice by treatment with the intestinal
RNA of mice of the same strain
JOURNAL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80
(2001)
REFERENCE 3 (bases 1 to 683)
AUTHORS Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.
and Su,C.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of
Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang
Le West Road, Xi'an 710032, China
LOCATION/Qualifiers
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CDS
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QY 580 TGGCGGTGGCGGATCCGATATCAGAGTCTCAGTCTCCATCTCCATCTCTCTCTCTCTCTCT 639
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QY 640 AGGCGAGAGGCGCCACCATATCTCCAGAGCCAGTGAAGTGTGTAGTATGGCGATAG 699
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QY 700 TTTTATGCACTGGTATCAGCAGAAACAGGACAGCCACCAACTCTCTCATCTATCGTGC 759
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DEFINITION sequence.
ACCESSION CK629396
VERSION CK629396.1 GI:45753871
KEYWORDS Apis mellifera (honey bee)
SOURCE Apis mellifera
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
1 (bases 1 to 872)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G., Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F., Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R., Ramos,R.G.P., Reis,L.P.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G., Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresafico,E.M., Espindola,P.S., Peco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, A.
Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 66
High quality sequence stop: 625.
Location/Qualifiers

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Matches 498; Conservative 0; Mismatches 183; Indels 27; Gaps 4;
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Db 329 TTGGTACCAACAGAGCCTGGATCTCTCCCGCAGACTCTCTGATTTATGACACATCCAACT 270
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QY 889 TCGTATACGTTTCGAGGGGGGACCCAGCTGGAATAAAGCGGCGGC 936
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DEFINITION sequence.
ACCESSION CK629846
VERSION CK629846.1 GI:45754321
KEYWORDS Apis mellifera (honey bee)
SOURCE


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Db |||
QY 612 AGTCTCCATCTTCTTTGGTGTCTCTCTAGGCGAGAGGCGCCACCATATCTCTGAGAGCCA 671
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QY 249 GCTCAAGTAT-----ACGTTACATATATTGGTACCAACAGAGCCTGGAT 205
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Db |||
QY 204 CCTCCCCAGACTCTGATTTATGACACATCCAACTGGCTCTGGAGTCCCTTTTCGCT 145
QY 792 TCAGTGGCAGTGGTCTGAGTACAGCTTCACTCTCACCATCGATCTGTGGAGGAAGATG 851
Db |||
QY 144 TCAGTGGCAGTGGTCTGGAGCTCTTATTTCTCTCAATCAACCGAAATGGAGGCTGAG 85
QY 852 ATGCTGCAGTGTATTCTGCTCCAAAGTATGGAAGTCCGTACACGTTCCGGAGGGGGA 911
Db |||
QY 84 ATGCTGCCACTTATTACTGCCAGAGTGGAGTGTTATCCGTACACGTTCCGGAGGGGGA 25
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QY 24 CCAAGCTGGAGCTGAACGGGCGG 1
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DEFINITION sequence.
ACCESSION CK629414
VERSION CK629414.1 GI:45753889
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
REFERENCE 1 (bases 1 to 1339)
AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresafico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
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TITLE Open reading frame ESTs - an efficient strategy for analysis of the
JOURNAL honey bee transcriptome
COMMENT Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 62
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Location/Qualifiers
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FEATURES
source

1. .1339
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Best Local Similarity 69.8%; Pred. No. 3.9e-71;
Matches 463; Conservative 0; Mismatches 174; Indels 26; Gaps 4;

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QY 395 ACT-PTAGACAATCTCCCAACACAGCCTATTTTGGAACCTTGCAGACTGACATCTCAGGA 453
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QY 454 TTCTGCCATTTTATTTGTGCAAGATCGGATGGTAAATTAACGGGTATTAATATGCTTTTGA 513
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QY 694 CGATAGTTTATGCACTGGTATCAGCAGAAAACAGCAGACGCCAACCAAACTCTCATCTA 753
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DEFINITION sequence.
ACCESSION CK629415
VERSION CK629415.1 GI:45753890
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera

REFERENCE 1 (bases 1 to 1419)

1. (bases 1 to 1419)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresafico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.

Zago, M.A., Soares, A.E.E., Bitondi, M.G., Espreafico, E.M., Espindola, F.S., Pato-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome

TITLE

Unpublished (2004)

JOURNAL

Molecular Genetic and Bioinformatics Laboratory

COMMENT

Department of Genetics, FMRP/USP, FUNDHERP

Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 39639300

Fax: +55 16 39639309

Email: wilsonj@usp.br

This sequence was derived from the FAPESP Genome Program

High quality sequence start: 63

High quality sequence stop: 605.

Location/Qualifiers

1. .1419

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/mol_type="mRNA"

/strain="Africanized"

/db_xref="taxon:7460"

/sex="female, worker"

/dev_stage="adult"

/clone_lib="AA0014"

/note="Organ: whole body"

Db 134 TATCCGTACACGTTCCGAGGGGGAGCCACAGCTGGAGCTGAACG 91

RESULT 10

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

602829112F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983962 5', mRNA sequence.

602829112F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983962 5', mRNA sequence.

602829112F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983962 5', mRNA sequence.

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602829112F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983962 5', mRNA sequence.

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DEFINITION	AM3-AP0011-151201-021-A08 AP0011 Apis mellifera cDNA, mRNA	672 bp	linear EST 26-MAR-2004
ACCESSION	CK633068		
VERSION	CK633068.1	GI:45757543	
KEYWORDS	EST.		
SOURCE	Apis mellifera (honey bee)		
ORGANISM	Apis mellifera		
REFERENCE	1 (bases 1 to 672)		
AUTHORS	Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M., Espindola, F.S., Faco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A. Jr.		
TITLE	Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Silva Jr, W. A. Molecular Genetic and Bioinformatics Laboratory Department of Genetics, FMRP/USP, FUNDHERP Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil Tel: +55 16 39639300 Fax: +55 16 39639309 Email: wilsonjr@usp.br This sequence was derived from the FAPESP Genome Program High quality sequence start: 100 High quality sequence stop: 629.		
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QY	644	CAGAGGCCACCATATCCTGCAGAGCCAGTGAAGTGTTCATAGTTATGCGCATAGTTT	703
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QY	764	AACCTAGAAATCTGGATCTCCCTGCAGGTCAGTGGCAGTGGTCTGAGTCAGATCTCACT	823
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QY	824	CTCACCATCGATCTCTGGAGGAGATGATGCTGCGAGTGATTAATCTCTGCGAAAGTATG	883
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LOCUS	CK633068		
DEFINITION	AM3-AP0011-151201-021-A08 AP0011 Apis mellifera cDNA, mRNA	672 bp	linear EST 26-MAR-2004
ACCESSION	CK633068		
VERSION	CK633068.1	GI:45757543	
KEYWORDS	EST.		
SOURCE	Apis mellifera (honey bee)		
ORGANISM	Apis mellifera		
REFERENCE	1 (bases 1 to 672)		
AUTHORS	Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M., Espindola, F.S., Faco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A. Jr.		
TITLE	Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Silva Jr, W. A. Molecular Genetic and Bioinformatics Laboratory Department of Genetics, FMRP/USP, FUNDHERP Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil Tel: +55 16 39639300 Fax: +55 16 39639309 Email: wilsonjr@usp.br This sequence was derived from the FAPESP Genome Program High quality sequence start: 100 High quality sequence stop: 629.		
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Best Local Similarity	69.5%;	Pred. No. 2.4e-68;	
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Db	224	TGATCGATTTTTCCTGGAGAGGGGAGTACTGAAATACAATGAGAAGTTCAAGGGCGAGGC	283
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Db 620 GATTATGACACATCCAACTGCTCTGAGTCCCACTTTGCTTCAGTGGC 671

RESULT 13

CK633069
LOCUS
DEFINITION
sequence.

CK633069
ACCESSION
VERSION
KEYWORDS
SOURCE

CK633069.1 GI:45757544
EST.
Apis mellifera (honey bee)

ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.

1 (bases 1 to 672)

Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresafico,E.M.,
Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome

Unpublished (2004)

Contact: Silva Jr, W. A.

Molecular Genetic and Bioinformatics Laboratory

Department of Genetics, FMRP/USP, FUNDHERP

Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 39639300

Fax: +55 16 39639309

Email: wilsonjr@usp.br

This sequence was derived from the FAPESP Genome Program

High quality sequence start: 100

High quality sequence stop: 629.

FEATURES

source

1. .672
/organism="Apis mellifera"
/mol_type="mRNA"
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/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="nupal"
/clone_lib="AP0011"
/note="Organ: whole body"

ORIGIN

Query Match 27.4%; Score 282.4; DB 7; Length 672;
Best Local Similarity 69.5%; Pred. No. 2.4e-68;

Matches 453; Conservative 0; Mismatches 171; Indels 28; Gaps 4;
QY 152 TCAGTGCCTCCGAGCGCCAGCCGATGCGCGAGGTCAAGCTGCAGAGTCAGGG-GC 210
Db 44 TGGCCCTTACATGCGCGGAGCGCGGACAGGGCCAGGTGAAGCTGCAGAGTCAGGGAAC 103
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Db 104 AGAAGTGGTAAAGCCGTGGGGCTTCAGCTGAAGTTGTCCGTGCAAGGCTTCTGGCTACAT 163
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QY 508 TTTGGACTACTGGGGCCAAAGGCACACTACGCTACCGTCTCTCAGGTGGAGCGGTTTCAGG 567
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QY 628 GGCTGTGCTCTTAGGGCAGAGGGCCACCATATCTCAGAGCCAGTGAAGGTGTGATAG 687
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QY 688 TTATGGCGATGATTTTATGACATGGTATCAGCAGAAACACAGGACAGCCACCAAACTCCT 747
Db 569 -----ACGTTACATATATTGTTACCAACAGAGCCCTGGATCTCTCCCGAGCTCCT 619
QY 748 CATCTATCGTGCATCCAACTAGAACTTGAGTCCCTGCGAGGTTTCAAGTGC 799
Db 620 GATTATGACACATCCAACTGCTCTGAGTCCCACTTTGCTTCAGTGGC 671

RESULT 14

BI107286

LOCUS

DEFINITION

musculus

ACCESSION

BI107286

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1108 row: i column: 22

BI107286 876 bp mRNA linear EST 26-JUN-2001
602894285F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5039325 5',
mRNA sequence.

GI:14558179

EST.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1108 row: i column: 22

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2005, 20:04:22 ; Search time 222 Seconds

(without alignments)
7591.734 Million cell updates/sec

Title: US-10-089-278-1

Perfect score: 1030

Sequence: 1 tccaccactctgactcaag.....ccagcccgagtcaggattatc 1030

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 5: /cgn2_6/ptodata/1/ina/PTCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	444	43.1	807	4	US-09-674-677-4
4	431.8	41.9	797	2	US-08-894-922A-13
5	424.2	41.2	894	4	US-09-486-814A-1
6	423.2	41.1	780	4	US-09-526-738A-3
7	417.8	40.6	771	4	US-09-526-738A-1
8	407.8	39.6	723	4	US-09-581-345-1
9	405.2	39.3	717	2	US-08-553-497A-17
10	403.2	39.1	1176	3	US-09-142-974B-3
11	403	39.1	810	2	US-08-552-507-1
12	402.4	39.1	864	3	US-09-423-439-47
13	401.6	39.0	1135	4	US-09-203-958A-3
14	400.4	38.9	996	4	US-09-742-693-27
15	398.8	38.7	996	2	US-08-894-922A-4
16	397.6	38.6	780	2	US-08-447-402-6
17	397.6	38.6	1010	3	US-09-070-408-1
18	395.2	38.4	717	3	US-09-142-974B-1
19	394.8	38.3	2019	3	US-09-423-439-31
20	394.8	38.3	2025	4	US-09-423-439-37
21	392.6	38.1	714	4	US-09-798-689-22
22	391.6	38.0	831	2	US-08-403-853-17
23	389.8	37.8	749	3	US-08-893-035A-46
24	389.4	37.8	1679	2	US-08-661-052-15
25	389.4	37.8	1679	3	US-09-188-082-15
26	389.4	37.8	1679	3	US-09-364-088-15
27	389.4	37.8	1679	3	US-09-102-716-15

28	389.2	37.8	756	2	US-08-797-689-17	Sequence 17, Appl
29	389.2	37.8	756	4	US-09-984-186-17	Sequence 17, Appl
30	389.2	37.8	1611	3	US-08-983-035A-37	Sequence 37, Appl
31	388	37.7	777	4	US-10-092-246-7	Sequence 7, Appl
32	388	37.7	777	4	US-10-096-246A-7	Sequence 19, Appl
33	385.6	37.4	732	2	US-08-553-497A-19	Sequence 6, Appl
34	384.8	37.4	777	4	US-10-092-246-6	Sequence 6, Appl
35	384.8	37.4	777	4	US-10-096-246A-6	Sequence 25, Appl
36	381.4	37.0	726	2	US-08-553-497A-25	Sequence 5, Appl
37	380.8	36.7	777	4	US-10-096-246-5	Sequence 27, Appl
38	378.4	36.7	777	4	US-10-096-246A-5	Sequence 43, Appl
39	378.4	36.7	726	2	US-08-553-497A-27	Sequence 50, Appl
40	377.6	36.7	843	3	US-09-423-439-43	Sequence 10, Appl
41	377.2	36.6	843	3	US-09-423-439-50	Sequence 4, Appl
42	369	35.8	1998	3	US-08-279-772A-7	
43	368.6	35.8	719	3	US-08-902-486-10	
44	368.6	35.8	720	3	US-10-092-246-4	
45	366.6	35.6	777	4	US-10-092-246-4	

ALIGNMENTS

RESULT 1

US-09-473-653-5
; Sequence 5, Application US/09473653
; Patent No. 6703015
; GENERAL INFORMATION:
; APPLICANT: Solomon, Beka
; APPLICANT: Prenkel, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: 00/20785
; CURRENT APPLICATION NUMBER: US/09/473,653
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: scFv 508F construct
US-09-473-653-5

Query Match		46.5%	Score 478.6; DB 4; Length 717;
Best Local Similarity		80.3%	Pred. No. 3.2e-117; Mismatches 119; Indels 27; Gaps 2;
Matches 597; Conservative 0;			
QY	186	AGGTCAAGCTGCAGCAGTCAGGGCTGAGCTGGTGAAGGCTGGGGTCTCAGTGAAGATTT	245
DB	2	AGGTCAACTGCAGGAGTCAGGGCTGAGCTGGTGAAGGCTGGGGTCTCAGTGAAGATTT	61
QY	246	CTGCAAGGGTCTGGCTACACATTCACCTGATTTATGGTATGAGCTGGGTGAAGACAGATC	305
DB	62	CCTGCAAGGGTCTGGCTACACATTCACCTGATTTATGGTATGAGCTGGGTGAAGACAGATC	121
QY	306	ATGCAAGAGTCTAGAGTGGATTTAGTACTTACTTACTTACTTACTTACTTACTTACTTACTT	365
DB	122	ATGCAAGAGTCTAGAGTGGATTTAGTACTTACTTACTTACTTACTTACTTACTTACTTACTT	181
QY	366	ACCAGAGTTCAAGGGCAAGGCCACAAATGACCTGTAGACAAATCCTCCAAACACAGCTATT	425
DB	182	ACCAGAGTTCAAGGGCAAGGCCACAAATGACCTGTAGACAAATCCTCCAAACACAGCTATT	241
QY	426	TGGAATCTGCCAGACTGACATCTGAGGATTTGCGCATTTATTTATTTGCAAGATCGGATG	485
DB	242	TGGAATCTGCCAGACTGACATCTGAGGATTTGCGCATTTATTTATTTGCAAGATCGGATG	301
QY	486	GTAAATACGGGTATTACTATGCTTTGGACTACTTGGGGCCCAAGGCACACTACGGTCACCGTCT	545

Db 302 CTATGTC-----TACTTTGACTACTGGGCGCAAGTGACCGGTCAACGGTCT 349
QY 546 CCTCAGGTGGAGCGGTTTCCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCAGC 605
Db 350 CCTCAGGTGGAGCGGTTTCCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCAGC 409
QY 606 TCACTCAGTCTCCATCTCTTTGGCTGTGTCTTAGGGCAGAGGGCCACCATATCTCGCA 665
Db 410 TCACTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACCATGCTGCA 469
QY 666 GAGCCAGTGAAGTGTGTAGTATGCGGATAGTATTTATGCACTGGTATCAGCAGAAAC 725
Db 470 GTGCCAGTCAAGTAT-----AAGTTACATGCACTGGTATCAGCAGAAAC 514
QY 726 CAGGACAGCCCAACCTCTCATCTATCGTGCATCCCACTAGATCTGGAGTCCCTG 785
Db 515 CAGGACCTCCCCCAAGATGATTTATGACATCCCAACTGGCTTCTGGAGTCCCTG 574
QY 786 CCAAGTTCAGTGGCAGTGGGTCTGAGTCAAGTTCATCTCTCAACATCGATCTGTGGAG 845
Db 575 CTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTATCTCTCAATCAGCAGCATGGAG 634
QY 846 AAGATGATCTCAGTGTATTACTGTCTGCAAGTATGGAAGATCCGTACAGTTCGGAG 905
Db 635 CTGAAGATGCTGCCACTTATTACTGCCATCAGCGGAGTAGTTACCCATTCACGTTCCGAG 694
QY 906 GGGGACCAAGCTGGAATAAAA 928
Db 695 GGGGCGCCAGCTGGAATAAAA 717

RESULT 2

US-08-894-922A-9
; Sequence 9, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITEHEAD, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894, 922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 60113/241261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 9:

FRAGME

; SEQUENCE CHARACTERISTICS:
; LENGTH: 891 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-08-894-922A-9
Query Match 43.5%; Score 448; DB 2; Length 891;
Best Local Similarity 76.2%; Pred. No. 46e-109;
Matches 613; Conservative 0; Mismatches 140; Indels 51; Gaps 3;
QY 141 CTGCCGAAGTTCGACTGCCCGAGCGGCCAGCGGCCATGCGCGAGGTCAAGTCTCAGC 200
Db 62 CAGCGCTGGATTGTTTACTCGCTGCCCAACCGCCATGCGCCAGGTGCGAGTCCAGC 121
QY 201 AGTCAGGGCTCAGCTGGTGGAGCCCTGGGGTCTCAGTGAAGATTTCCTTCGCAAGGTTCTG 260
Db 122 AGTCTGGGGCTGAACCTGGTGAAGCCCTGGGCCCTTCTGTGAAGCTGTCTCTCAAGGCTTCCG 191
QY 261 GCTACACATTCATCTGATATGTTATGCTGAGTGGGTGAAACAGAGTCAATGCAAGAGTCTAG 320
Db 182 ACTACACCTTCAACAGTTATGAGTGCACTGGGTGAGCAGAGGCTTGCACAGGCTTGG 241
QY 321 AGTGGATTGGACTTATTAGTACTTACTATGTTGATCTCTAGTTCATCAACAGAGGTTCAGG 380
Db 242 AGTGGATTGGAGAGATTATCTTACCAACGGTCTGTTATTTACATGAGAGTTCAGA 301
QY 381 GCAAGGCCAATGACTGTAGCAAAATCTCAACACAGCCCTATTGGAACTTGCAGAC 440
Db 302 GCAAGGCCACACTGACTGTAGCAAAATCTTCCAGTACAGCCCTACATGCGAGCTCAGCAGC 361
QY 441 TGACATCTCAGGATTCCTGCCATTTATTATTGTGCAAGATCGGATGTTAATTACGGGTATT 500
Db 362 TGACATCTCAGGACTCTCGGCTCTATTACTGTGCAAGCGGTATGGTAAT-----412
QY 501 ACTATGCTTTGGACTACTGGGGCCCAAGGCATACCGTCAACCGTCTCTCAGGTGGAGCG 560
Db 413 -----CCTTTGACTACTGGGGCCCAAGGCACCGGTCAACCGTCTCTCTCA-----456
QY 561 GTTCAGCGGAGGTGGCTCTCGGGTGGCGGATCGGATATCGAGTCACTCAGTCTCCAT 620
Db 457 -----CGAATGGATATAAAGGGGACATCGAGCTCACTCCAGTCTCCAG 496
QY 621 CTTCTTTGGCTGTCTCTAGGCGCAGAGGGCCACCATATCTCTCAGAGCCAGTGAAGTG 680
Db 497 ATTCTTTGGCTGTCTCTAGGCGCAGAGGGCCACCATATCTCTCAGAGCCAGTGAAGTG 556
QY 681 TTGATAGTTATGGCGATAGTTTATGCACTGGTATCAGCAGAAACAGAGCAGCCACCCA 740
Db 557 TTGATAGTTATGGCAATAGTTTATGCACTGGTATCAGCAGAAACAGAGCAGCCACCCA 616
QY 741 AACTCCTCATCTATCGTGCATCCAACTAGATCTGGAGTCCCTGCGCAGTTCAGTGGCA 800
Db 617 AACTCCTCATCTATCGTGCATCCAACTAGATCTGGAGTTCCTGCGCAGTTCAGTGGCA 676
QY 801 GTGGGTCTCAGTCAAGTTCCTCTCACCATCGATCTCTGGAGGAGATGATGCTGCAG 860
Db 677 CTGGGTCTAGGACAGACTTCACTTCACTTCACTTAACTCTGTGGAGGCTGATGTTGCCA 736
QY 861 TGTATTACTGTCTGCAAAAGTATGGAAGATCC-----GTACAGTTCGAGGGGGGACCA 914
Db 737 CCTATTATTGTCAACAAAGTATGAGTATCCGTACATGTACAGTTCGAGGGGGGGACCA 796
QY 915 AGCTGGAATAAAGCGGGCGCG 938
Db 797 AGCTCGAGATCAACGGGATCCG 820

RESULT 3

US-09-674-677-4
; Sequence 4, Application US/09674677
; Patent No. 6562622

Query Match	43.1%	Score 444;	DB 4;	Length 807;
Best Local Similarity	76.4%;	Pred. No. 5.1e-108;		
Matches 584;	Conservative 0;	Mismatches 150;	Indels 30;	Gaps 2;
Qy	177	CCATGGCCGAGGTC	AAAGCTGCAGCAGTC	CAGGCGCTGAGCTGGTCAGGCGCTGGGCTCTCAG 236
Db	1	CCATGGCCGATG	TGAAGCTTCAGGAGTC	CAGGCGCTGAGCTGGTCAGGCGCGGGGCTCTCAG 60
Qy	237	TGAAGATTTCCTG	CAAGGGTTCTGGCTAC	ACATTCACCTGATATTGGTATGAGCTGGGTGA 296
Db	61	TGAAGATTACTGC	AGGGTTCCGGCTAC	ACATTCACCTGATATTGCTATGCAATGGGTGA 120
Qy	297	AACAGAGTCATGC	AAAGAGTCTAGAGTGG	ATTGGACTTATTAGTACTTACTATGCTGATC 356
Db	121	AGCAGAGTCATGC	AAAGAGTCTAGAGTGG	ATTGGACTTATTAGTAAATTCCTTTGGTAA 180
Qy	357	CTAGTTTAAACCA	CCAGAGGTTCAAGGG	CAAGGCCAACATGACTGTGTAGACAAATCTCTCCAACA 416
Db	181	CAAACTACAACCA	GAAGTTTGAGGCCA	AGGCCAACATGACTGTGTAGACAAATCTCTCCAACA 240
Qy	417	CAGGCTATTTGGA	ACTTGCAGACTGAC	ACTGTAGGATTCGCCACTTATTATTGTGCGAA 476
Db	241	CAGGCTATTTGGA	ACTTGGCAGATTGAC	ATCTGAGGATTCGCCACTTATTACTGTGCGAA 300
Qy	477	GATCGGATGGTA	ATTACGGGTATTACT	ATGCTTTGGGACTCTGGGGCCAAAGGCATACGG 536
Db	301	GA-----GTG	ATCGACTTGGTCTCT	TGATGCTGGGGCCAAAGGACCAACGG 345
Qy	537	TCACCGTCTCCTC	AGGTGGAGGCGGTT	CAGCGGAGGTGGCTCTGGCGGTGGCGGATCGG 596
Db	346	TCACCGTCTCCTC	AGGTGGAGGCGGTT	CAGCGGAGGTGGCTCTGGCGGTGGCGGATCGG 405
Qy	597	ATATCGAGCTC	ACTCAGTCTCCATCT	CTTTTGGCTGTGTCTGTAGGGCAGAGGGCCACCA 656
Db	406	ACATTTGTGTG	ACCCAAATCTCCAG	CAATCTATGTTCCGATCTCCAGGGGAGAAAGTCCACCA 465
Qy	657	TATCTGCGAGCG	CAGTGAAGTCTTGAT	AGTTATGGCGATAGTTTATGCACGTGGTATC 716
Db	466	TGACCTCGAGTGC	CACTCAGTGT-----	CAGGTACGTGCACGTGGTACC 510
Qy	717	AGCAGAAAC	CAGGACGCCACCC	AAACTCTCATCTATCGTGCATCCAACTAGAAATCTG 776
Db	511	AACAGAAGT	CAGGCACCTCCCC	AAAAGATGGATTTATGACATCCAACTAGCCTCTG 570
Qy	777	GAGTCCCTGCC	AGGTTCAGTGGC	AGTGGGTCTGAGTCAGACTTCTCAACATCGATC 836
Db	571	GAGTCCCTGCT	CGCTTCAGTGGC	AGTGGGTCTGAGTCACTCTCTCACAATCAGCA 630
Qy	837	CTGTGGAGGA	AGATGATGCTGCA	GTGATTACTGCTCTGCAAGTATGGAAGATCCGTACA 896

	Query Match	41.9%	Score 431.8;	DB 2;	Length 797;
	Best Local Similarity	77.2%;	Pred. No. 8.8e-105;		
	Matches 586;	Conservative 0;	Mismatches 122;	Indels 51;	Gaps 3
Qy	186	AGGTCAAGCTGCAGCAGCTCAGGGGCTCAGCTGGTGGAGCCCTGGGGTCTCTCAGTGAAGATTT	245		
Db	13	AGGTGCAGCTGCAGCAGCTCTGGGGCTGAACTGGTGAAGCCCTGGGGCTTCTGTGAAGCTGT	72		
Qy	246	CTGTCAAGGGTTCTGGCTTACACATTCACCTGATTAATGGTATGAGCTGGGTGAAACAGAGTC	305		
Db	73	CTGTCAAGGGTTCCGATTCACACCTTCACAGTTATTGGATGCACTGGGTGAAGCAGAGGC	132		
Qy	306	ATGCARAGAGCTAGAGCTGGATTGGACTTATTAGTACTTACTATGGTGTGATCCTAGTTACA	365		
Db	133	CTGGCAAGGCCCTTGGTGGATTGGAGAGATTAACTCTACCAAGCTGCTGTTATTATTACA	192		
Qy	366	ACCAGAGGTTCAAGGGCAAGGCCAACATGACTGTAGACAAATCTCCAACACAGCCCTATT	425		

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;
; LOCATION: (436)..(528)
; OTHER INFORMATION: Encoding a linker sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (838)..(891)
; OTHER INFORMATION: Encoding a TAIL sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(894)
; OTHER INFORMATION: strandedness: double-stranded
;
US-09-486-814A-1

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Query Match 41.2%; Score 424.2; DB 4; Length 894;
Best Local Similarity 73.8%; Pred. No. 9.5e-103;
Matches 597; Conservative 0; Mismatches 173; Indels 39; Gaps 3;

QY	138	CACTGCGGAGGTTTCGACTGCGGAGCGCGCCAGCGCGCCATGCGCGGAGGTCAAGCTGC	197
DB	71	CAATTCTTTAGTTGTTCTTTCTATGCGCGCCAGCGCGCCATGCGCGGAGGTCAAGCTGC	130
QY	198	AGCAGTCAGGCGGTGAGCTGGTGGGCTCTCAGTGAAGATTCTCTCAAGGGTT	257
DB	131	AGAGTCAGGACCTGAGCTGGAGAGCCTGGGCTTCAGTGAAGATATCTTGCAGGCTT	190
QY	258	CTGGCTACACATTCACCTGATATGATGAGCTGGGTGAAACAGAGTCATGCAAGAGTC	317
DB	191	CTGGTTACTCAITTCACCTGGCTACACATCAAGTGGGTGAAACAGAGCAATGGAAGAGCC	250
QY	318	TAGAGTGGATTGGACTTATTAGTACTTACTATGGTGATCCTAGTTACACACAGAGTTCA	377
DB	251	TTGAGTGGATTGGATATATTATCTTCAATGGTGGTACTGGCTACACACAGAGTTCA	310
QY	378	AGGGCAAGGCCACATGACTGTAGACAAATCCTCAACACAGAGCTATTGGAACTTGGCCA	437
DB	311	AGAGCAGGCCACATTCAGTGTAGACAAATCCTCAGCAGAGCTACATGCAACTGAGCA	370
QY	438	GACTGACATCTGAGGATCTGCCATTTATTTGTCAGAGATCGGATGTTAATACGGGT	497
DB	371	GCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGACTG-----	414
QY	498	ATTACTATCTGTTGGACTACTGGGCGCAAGGCACTACGGTCAACCGTCTCTCAGGTGGAG	557
DB	415	-----GGACTTGACTACTGGGCGCAAGGCAACACGGTCAACCGTCTCTCAGGTGGAG	466
QY	558	GCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGCTCACTCAGTCTC	617
DB	467	GCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGCTCACTCAGTCTC	526
QY	618	CATCTTTTGGCTGTCTCTAGGCGAGGCGCCACCATATCTCTGAGAGCCAGTGAAA	677
DB	527	CAACCACTATGGTGCATCTCCCGGGGAGAAGATCACTATCACTGCAGTGCAGCTCAA	586
QY	678	GTGTTGATAGTTATGGCGATGTTTTATGCACTGGTATCAGCAGAAACAGAGCAGCCAC	737
DB	587	GTAT-----AAGTTCCAAATTAATTGATTTGGTATCAGCAGAAACAGAGTCTTCCC	637
QY	738	CAAACTCTCATCTATCGTGCATCCAACTAGAACTAGAGTCCCTGCCAGGTTCAAGTG	797
DB	638	CTAACTCTGATTTATAGGACATCAATCTGGCTCTGGAATCCCGAGTCTCGTTCAGTG	697
QY	798	GCACTGGGCTCTGAGTCAGACTTCCTCCTCAGCATCGATCCTGTGGAGGAGATGATGCTG	857
DB	698	GCACTGGGCTCTGGGACCTCTTACTCTCACAATTTGGCACCACCATGGAGGCTGAAGATGTTG	757
QY	858	CAGTGTATTACTCTCTGCA-----AAGTATGGAAGATCCGTACACGTTCCGGAGGGGGA	911
DB	758	CACTTACTACTCCAGCAGGGTAGTAGTATACCAAGCATATTACGTTCTGGTCTGGGA	817
QY	912	CAAGCTGGAAATATAAACCGGCGCGCA	940
DB	818	CAAGTTGGAATATAAACCGGCGCGCA	846

RESULT 5
US-09-486-814A-1
; Sequence 1, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 6562599io
; APPLICANT: YAMAMOTO, Hiroko
; APPLICANT: TOHDOH, Naoki
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486, 814A
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
; FEATURE:
; OTHER INFORMATION: Clone: pZeoSVic9
; NAME/KEY: CDS
; LOCATION: (1)..(891)
; OTHER INFORMATION: Identification Method: E
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(111)
; OTHER INFORMATION: Encoding PRE-HV sequence
; FEATURE:
; NAME/KEY: misc_feature

Query Match	40.6%;	Score 417.8;	DB 4;	Length 771;
Best Local Similarity	74.8%;	Pred. No. 4.5e-101;		
Matches 565;	Conservative 0;	Mismatches 157;	Indels 33;	Gaps 2;
Qy	186	AGGCTCAAGCTGCAGCAGTCAAGGGGCTCAGCTGGTGAAGGCTCGGGTCTCAGTGAAGATT	245	
Db	2	AGGTCAAACTGCAAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCTCAGTGAAGATGT	61	
Qy	246	CCTGCAAGGTTCTGGCTACACATTCACCTGATTATGGTATGATGAGCTGGGTGAAACAGAGTC	305	
Db	62	CCTGCAAGACTTCTGGCTACACCTTTACTAGCTACTGGATGAATCGGTAAACAGAGGC	121	
Qy	306	ATGCAAGAGCTTAGAGTGAATTGGACTTATTAGTACTTACTATGTTGATCCTTAGTTACA	365	
Db	122	CTGGACAGGGTCTGGGAATGGATTGGATACATTAACTCCTACCTGGTTACTAAGTACA	181	
Qy	366	ACCAGAGGTTCAAGGSCAAGGCCACAATGACTGAGACAAATCCTCAACACAGCCTATT	425	
Db	182	ATCAGAAGTTCAAGHCAAGGCCACATTGACTGCGACAAATCCTCAGCACGGCCTACA	241	
Qy	426	TGGAACCTGCGACACTGACATCTGAGGATTCTGCCATTCTTATTATGTCGAAGATCGGATG	485	
Db	242	TGCAACTGAGCAGCCTGCACCAATGTGGACTCTGCACTTCTATTATGTTACAA	292	
Qy	486	GTAATTACGGGTATTTACTATGCTTTTGGACTCTGCGGGCCAAAGGACTACGGTCAACCGTCT	545	
Db	293	-----CTGGTTACTCTTATTTTGACTACTCTGGGGCCAAAGGACACACGGTCAACCGTCT	343	
Qy	546	CCTCAGGTGAGCGGTTTCAGGGGAGGTGGCTCTCGCGTGGCGGATCGGATATCGAGC	605	
Db	344	CCTCAGGTGAGCGGTTTCAGGGGAGGTGGCTCTCGCGTGGCGGATCGGATATCGAGC	403	
Qy	606	TCACTCAGTCTCCATCTTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCCTGCA	665	
Db	404	TCACTCAGTCTCAGCAATCAATGTCTGCATCTCCAGGGGAGAGGTCAACATTAACCTGCA	463	
Qy	666	GAGCCAGTGAAGTGTGATGATTATGGCGATAGTTTTATGCACTGGTATCAGCAGAAAC	725	
Db	464	GTGCCAGCTCAAGTGT-----AAATTACATGCATCTGGTTCCAGCAGAAAGC	508	
Qy	726	CAGGACAGCCACCAACCTCTCATCTATGTCATCCCAACCTAGAACTCGGAGTCCCTG	785	
Db	509	CAGGCACTTCTCCAAACTCTGGATTTCTAGCACTCCCAACCTCTGGAGTCCCTG	568	
Qy	786	CCAGGTTTCAAGTGGCAGTGGGTCTGAGTCAGACTTTCATCTCACCATCGATCTCTGTGGAGG	845	
Db	569	CTCGCTTCAGTGGCAGTGGATCTGGGACCTCTTACTCTCTCAATCAGCCGGATGGAGG	628	
Qy	846	AAGATGATGTCGAGTGTATTACTGTCTGCAAAAGTATGGAAGATCCGTACACTTCGGAG	905	
Db	629	CTGAAGATGCTGCACCTTATTCTGCGCAGCAAGGAGTAGTTACCATACACTCAGCTTCGGAG	688	


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, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
, HYPOTHETICAL: NO
, ANTI-SENSE: NO
, FRAGMENT TYPE: N-terminal
, ORIGINAL SOURCE:
, ORGANISM: mouse
, STRAIN: Balb/c
, DEVELOPMENTAL STAGE: adult
, TISSUE TYPE: splenocyte
, IMMEDIATE SOURCE:
, CLONE: 4 B 2
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 1..717
US-08-553-497A-17

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Query Match	39.3%	Score	405.2	DB 2	Length	717			
Best Local Similarity	73.6%	Pred. No.	9.7e-98						
Matches	534	Conservative	0	Mismatches	183	Indels	9	Gaps	1
QY	185	GAGGTCAAGCTGCAGCAGTGCAGGGCTGAGCTGCTGGTGGAGCTGGGTCTCAGTCAAGATT	244						
DB	1	GAGGTGAAGCTGCAGGAGTCTGGGGGAGACTTAGTGAAGCCTGGAGGGTCCCTGAAACTC	60						
QY	245	TCCTGCAAGGGTTCTGGCTACACATTCACTGATTAATGTTATGCTATGAGCTGGGTGAAACAGAGT	304						
DB	61	TCCTGTGCAGCCTCTCGATTACATTTTCAGTAGCTATGGCATGTCTTGGTTTCGCAGACT	120						
QY	305	CATGCAAAAGTCTAGAGTGGATTGGACTTATTAGTACTTACTATGTTGATCTCTAGTTAC	364						
DB	121	CCAGACAAGAGCTGGAGTCTGTGCGAACCAATTAGTAGTGGTGTGCTTACATCTACTAT	180						
QY	365	AACCAGAGGTTCAAGGCGAAGGCCACAAATGACTCTAGACAAATCCTCCAACACAGCCTAT	424						
DB	181	CCAGACAGTGTGAAGGGCGATTCCCATCTCCAGAGACAATGCTCAAGAACCCCTGTAC	240						
QY	425	TTGGAACTTCCAGACTGACATCTGAGGATTCGCCATTTATTATTGTGCAAGATCGGAT	484						
DB	241	CTGCAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGA-----	294						
QY	485	GGTAAATTACGGGTATTACTATGCTTTGGACTACTTGGGCCCAAGGCACTACGGTCACCGTC	544						
DB	295	---CTTGAAAACCGGGACTATGCTTTTGGACTACTGGGGCCAAAGGACCAAGGTCACCGTC	351						
QY	545	TCCTCAGGTGGAGCGCGTTCAAGCGGAGGTGGCTCTGGCGGTGCGGATCGGATATCGAG	604						
DB	352	TCCTCAGTGGCGGTGGCTCGGGCGGTGGTGGGTGGGTGGCGCGGATCTGACATTGAG	411						
QY	605	CTCAGTCACTCCATCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACATATCTCTGC	664						
DB	412	CTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTCTAGGGCAGAGGGCCACCATATCTCTGC	471						
QY	665	AGAGCCAGTCAAAAGTGTGATGTTATGGCGATAGTTTATGCACTGCTATCAGCAGAA	724						
DB	472	AAGACAGCCAAAGTGTGATATGATGGTGATGTTATGAACTGGTACCAACAGAA	531						
QY	725	CCAGGACAGCCACCCAAACTCCTCATCTATCGTGCATCCAACTAGAACTCTGGAGTCCCT	784						
DB	532	CCAGGACAGCCACCCAAACTCCTCATCTATGCTCGATCCAACTCTAGAACTCTGGGTCCCT	591						
QY	785	GCCAGGTTCACTGGCAGTGGGTCTGAGTCAGACTTCTACTCTCACCATCGATCTCTGTGGAG	844						
DB	592	GCCAGGTTTATGGCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCATCTCTGTGGAG	651						
QY	845	GAAGATGATGCTGCAGTGTATTACTGTCTGCAAAAGTATGGAAGTCCGTACACCGTTCGGA	904						
DB	652	GAGATGATATTGCAATGTATTTCTGTGCGAAGTAGGAGGTTCCGTGGTCTGCTCGGT	711						
QY	905	GGGGGG	910						
DB	712	GGAGGG	717						

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RESULT 10
US-09-142-974B-3
; Sequence 3, Application US/09142974B
; Patent No. 6451995
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Fen
; APPLICANT: Rivlin, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside Gb2
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: MSK.P-013-USNP
; CURRENT APPLICATION NUMBER: US/09/142,974B
; CURRENT FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/US97/04427
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,703
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: 5fll-scFv-streptavidin
; NAME/KEY: unsure
; LOCATION: (37)
; NAME/KEY: unsure
; LOCATION: (79)
; US-09-142-974B-3

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Query Match	39.1%;	Score 403.2;	DB 3;	Length 1176;
Best Local Similarity	73.5%;	Pred. No. 4e-97;		
Matches	554;	Conservative 0;	Mismatches 170;	Indels 30; Gaps 2
Qy	186	AGGTCAAGCTGCAGCAGTCAAGGGCTGAGCTGGTGGAGCCCTGGGGTCTCACTGAAGATT	245	
Db	2	AGGTGAACCTGCAGCAGTCAAGGACCTGAACCTGGTGNAGCCCTGGGGCTTCACTGAAGATAT	61	
Qy	246	CCTGCAAGGGTCTTGGCTACACATTCCTACTGATTATGGTATGAGCTGGTGGTGAACAGAGTC	305	
Db	62	CCTGCAAGACTTCTGGANACAAATTCCTCAATACACCTGCACTGGGTGAAGCAGAGCC	121	
Qy	306	ATGCAAGAGCTAGAGTGGATTGGACTTATTAGTACTTACTATGGTGATCCTAGTTACA	365	
Db	122	ATGGAAGAGCCTTGAGTGGATTGGAGGTATTAATCTTAACATGGTGGTACTAAGTTACA	181	
Qy	366	ACCAGAGGTTCAAGGGCAAGGCCACATGACTGTAGACAAATCCTCCAACACAGCCATT	425	
Db	182	AGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCTCTCCAGCACAGCCTTACA	241	
Qy	426	TGGAACCTTGCAGACTGACATCTGAGAGATTCTGCGCATTTATATTGTGCAAGATCGGATG	485	
Db	242	TGGAGCTCCGAGCCTGACATCTGAGGATCTGCAGTCTATTACTGTGCAAGA	294	
Qy	486	GTAAATTACGGGTATTACTATGCTTTGGACTACTTGGGGCCAAAGGCACATCGGTACCGTCT	545	
Db	295	-----GATACTACGGTCCCGTTTGCTTTACTTGGGTCCAAGGACCAACGGTCAACCGTCT	346	
Qy	546	CCTCAGTGCAGCGGTTCAAGGCGGAGTGGCTCTGCGGGTGGCGGATCCGATATCCAGC	605	
Db	347	CCTCAGTGCAGCGGTTCAAGGCGGAGTGGCTCTGCGGGTGGCGGATCCGACATCGAGC	406	
Qy	606	TCACTCAGTCTCCATCTTCTTTGGCTGTGCTCTTAGGGCAGAGGGCCACCATATCCTGCA	665	
Db	407	TCACTCAGTCTCCAGCAATCATGCTGCACTCTCCAGGGGAGAGGTCACCATGACCTGCA	466	
Qy	666	GAGCCAGTGAAGTGTTGATAGTTATGGCGATAGTTTTATGCACTGGTATCAGCAGAAAC	725	

PRIOR APPLICATION DATA:									
APPLICATION NUMBER: PCT/GB98/01294									
FILING DATE: 05-MAY-1998									
APPLICATION NUMBER: GB 9709421.3									
FILING DATE: 10-MAY-1997									
INFORMATION FOR SEQ ID NO: 47:									
SEQUENCE CHARACTERISTICS:									
LENGTH: 864 base pairs									
TYPE: nucleic acid									
STRANDEDNESS: single									
TOPOLOGY: linear									
MOLECULE TYPE: other nucleic acid									
SEQUENCE DESCRIPTION: SEQ ID NO: 47:									
US-09-423-439-47									

Query Match	39.1%;	Score 402.4;	DB 3;	Length 864;
Best Local Similarity	71.6%;	Pred. No. 5.8e-97;		
Matches	574;	Conservative	0;	Mismatches 216; Indels 12; Gaps 3;

Qy	137	ACCACTGCCGAGTTTCAGCTGCCGCGAGCGGCCAGCGGCATATGCGCGAGGTCAAGCTG	196
Db	19	ACGCGACCGCTGATGTTGTTATTACTCGCTGCCAACCCAGCATGGCCAGGTCCAACTG	78
Qy	197	CAGCAGTCAGGGCTGAGCTGGTCAGCGCTGGGGTCTCAGTGAGATTTCCTGCAAGGCT	256
Db	79	CAGCAGCTGGGGCTGAACCTGGTGAAGCTTGGGGCTTCAGTGCAGCTGTCTCTGCAAGCT	138
Qy	257	TCTGGCTACACATTCACTGATTTATGGTATGAGCTGGGTGAAACAGAGTCATGCAAAAGT	316
Db	139	TCTGGCTACACCTTCACCGGCTACTGGATACACTGGGTGAAGCAGAGGCTTGGACAAGC	198
Qy	317	CTAGAGTGGATTGGACTTATTAGTATTTAGTATTTATGGTGTATCTTAGTACAACAGAGGTTTC	376
Db	199	CTTGAGTGGATTGGAGAGGTTTAACTCTAGTACCGGTCTGTTCTGACTACAATGAGAAGTTC	258
Qy	377	AAGGGCAAGGCCCAATGACTGTAGACAAATCTCTCAACACAGGCTATTGTGAACTTGCC	436
Db	259	AAGAAACAAGGCCCACTGACTGTAGACAAATCTCTCAACACAGGCTATCATGCAACTCAGC	318
Qy	437	AGACTGACATCTGAGGATTCGCCATTATTTATTTGTGCAAGATCGGATGGTAAATTACGGG	496
Db	319	AGCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA---GAGAGGGCTATGGT	375
Qy	497	TATTACTATGCTTTGGACTACTGGGGCCAAGGCACTACGGTCAACCGTCTCTCTCAGGTGGA	556
Db	376	TACGACGATGCTATGGACTACTGGGGCCAAGGGACCAAGGTCACCGTCTCTCAGGTGCG	435
Qy	557	GGCGGTTCAGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGCTCACTCAGTCT	616
Db	436	GGTGGCTCGGGCGGTGGGTGGGTGGCGCGGATCTGCATTTGAGCTCTCAGCTCT	495
Qy	617	CCATCTTTCTTTGGCTGTGCTCTAGGGCAGAGGGCCACCATATCTTCAGAGCAGGTCGAA	676
Db	496	CCATCTCTCTGGCTGTGTCAGAGGAGAGAGGTTCACCATGAGCTGCAATTCAGTCAG	555
Qy	677	AGTGT-----TGATAGTTATGGCGATAGTTTATGCACTGGTATCAGCAGAAAACCAAGGA	730
Db	556	AGTCTCTCAACAGTAGAACCCGAAAGAACTACTTTGGCTTGGTACCAGCAGAGACCAAGG	615
Qy	731	CAGCCACCCAAATCTCTCATCTATCTGTGCATCCAACTAGAAATCTGAGATCCCTGCCAGG	790
Db	616	CAGTCTCTAAACTGCTGATCTATTGGGCATCCACTAGGACATCTGGGGTCCCTGATCGC	675
Qy	791	TTCACTGGCAGTGGGTCTGAGTCAGACTTCACTCTCCATTCGATCTGTGTGGAGGAGAT	850
Db	676	TTCAAGGAGTGGATCTGGGACAGATTTCATCTCTCACCATCAGAGGTGTCAGGCTGAA	735
Qy	851	GATGCTGCAGTGTATTACTGTCTGCCAAGTATGGAAGATCCGTTACAGTTCGGAGGGGG	910
Db	736	GACCTGGCAATTATTACTGCAAGCAATCT---TATACTCTTCGAGCGTTGGTGAGGC	792
Qy	911	ACCAAGCTGGAAATAAAACGGG	932

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Db 746 ACCGGCTTAATCTATCTGGTGTCTAACTGGATCTGGAGTCCCTGACAGGTTCACTGGC 805
Qy 800 AGTGGGTCTGAGTCAGACACTTCACTCTCACCATCGATCCTGTGGAGGAAGATGATGTGCA 859
Db 806 AGTGGATCAGGACAGATTTTCACACTGAAATCAGCAGAGTGGAGGCTGAGGATTTGGGA 865
Qy 860 GTGTATTACTGTCTGAAAGATGGAAGATCCGTACACGTTCCGAGGGGGGACCAAGCTG 919
Db 866 ATTTATTATTGCTGGCAAGGTGCACATTTTCTCAGACGTTCCGTGGAGGCCACCAAGCTG 925
Qy 920 GAATTAACCG 931
Db 926 GAAATCAACCG 937

RESULT 14
US-09-742-693-27
; Sequence 27, Application US/09742693
; Patent No. 6579842
; GENERAL INFORMATION:
; APPLICANT: HOWELL, Steven
; APPLICANT: LITTLE, Julie C.
; APPLICANT: VAN DER LOGT, Cornelis P.
; APPLICANT: PARRY, Neil J.
; TITLE OF INVENTION: METHOD OF TREATING FABRICS
; FILE REFERENCE: C7536 (V)
; CURRENT APPLICATION NUMBER: US/09/742,693
; PRIOR FILING DATE: 2001-06-15
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 27
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-742-693-27

Query Match 38.9%; Score 400.4; DB 4; Length 996;
Best Local Similarity 70.4%; Pred. No. 2.1e-96;
Matches 611; Conservative 0; Mismatches 191; Indels 66; Gaps 3;

Qy 137 ACCACTGCCGAAGTTTCGACTGCCGAGCGGCCCGCCATGGCCGAGGTCAAGCTG 196
Db 58 ACGGACGCGCTGGATTGTTTATTACTGCTGCTGCCAACCGGCCATGGCCAGGTGCAGCTG 117
Qy 197 CAGCAGTCAGGGCTGAGCTGGTGAAGCCTGGGCTCTAGTGAAGATTCTCTCAAGGTT 256
Db 118 CAGCAGTCGGGCTGAACCTGGTGAAGCCTGGGCTCTCTGAAGCTGCTCTCAAGGCT 177
Qy 257 TCTGGCTACACATTCACTGATTATGGTATGATGAGTGGGTGAACAGAGTCAATGCAAGAGT 316
Db 178 TCCGACTACACCTTCCAGCTTATGGATGATGCTGGGTGAAGCAGAGGCTGACAGGC 237
Qy 317 CTAGAGTGGATTGGACTTATTAGTACTTACTATGGTGAATCCTAGTTACAAACAGAGGTT 376
Db 238 CTTGAGTGGATTGGAGAGATTAATCCTACCAACGGTCTGTTATTACATGAGAGTTT 297
Qy 377 AAGGCCAAGCCCAATGACTGTAGACAAATCTCCACACAGCTTATTGGAACTTGC 436
Db 298 AAGAGCAAGCCCACTGACTGTAGACAAATCTTCCAGTACAGCCCTACATGCAAGCTCAGC 357
Qy 437 AGACTGACATCTGAGGATTTCTGCCATTATTATTGTGCAAGATCGGATGGTAAATTACGGG 496
Db 358 AGCTGACATCTGAGGACTCTGGGCTATTACTGTGCAAGACGCTATGTTACTCTTTT 417
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Qy 497 TATTACTATG----- 506
Db 418 GACTACTGGGCCAAGGGACCAACGGTCAACCGTCTCTCTATAATAAGAGCTATGGAGCTT 477
Qy 507 -----CTTTGGACTACTGGGCCAAGGCACCTACGGTCAACCGTCTCTCTCAGTGGAGGC 559
Db 478 GCATGCAAAATTTATTTCAGAGGAGACAGTCATAATGAAATACCTATTGGCTACGGCAGCC 537
Qy 560 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGA---TCGGATATCCAGCTCACTCACTCT 616
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Qy 617 CCATCTCTTTGGCTGTCTCTAGGGCAGAGGGCCACCATATCTTCGACAGAGCCAGTGAA 676
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Qy 677 AGTGTGATAGTATGCGCATAGTTTATGCACTGCTATCAGCAGAAACAGAGACAGCCA 736
Db 658 AGTGTGATAGTATGCGCAATAGTTTATGCACTGCTATCAGCAGAAACAGAGACAGCCA 717
Qy 737 CCAAACTCTCATCTATCGTCATCAACCTAGAAATCTGGAGTCCCTGCCAGGTTTCAGT 796
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Db 778 GGCAGTGGGTGAGTCAGACTTCAACCTCAACATTAATCTCTGGAGGCTGATGATGTT 837
Qy 857 GCAGTGTATTACTCTCTGCAAAAGTATGGAAGATCC-----GTACACGTTTCGGAGGGGG 910
Db 838 GCAACCTATTATTGTCAAAAGTATGATGATTCCTATACATGTACACGTTTCGGAGGGGG 897
Qy 911 ACCAAGCTGGAATAAAACGGCGGCCG 938
Db 898 ACCAAGCTCGAGATCAACCGGGATCCG 925

RESULT 15
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; Sequence 4, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITELAM, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
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FRAGME

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; REFERENCE/DOCKET NUMBER: 60113/241261
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 996 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; US-08-894-922A-4

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Query Match	38.7%;	Score 398.8;	DB 2;	Length 996;
Best Local Similarity	70.3%;	Pred. No. 5.5e-96;		
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QY	137	ACCACCTGCCGAAGTTTCAGACTGCCCGAGCGGCCAGCGGCCCATGGCGAGGTCGAAGCTG	196	
Db	58	ACGGCAGCCCTGGATTGTTATTACTCGCTGCCCAACGGGCCATGGCCAGGTGACGCTG	117	
QY	197	CAGCAGTTCAGGGCTGAGCTGGTGAGGCCCTGGGGTCTCAGTGAAGATTTCTTGCAGAGGT	256	
Db	118	CAGCAGTCTGGGGCTGAACCTGGTGAAGCCCTGGGCTCTCTGTGAAGCTGTCTCTGCAAGGCT	177	
QY	257	TCCTGGCTACACATTCACCTGATTAAGTGTATGAGCTGGGTGAACAGAGTTCATGCAAGAGT	316	
Db	178	TCCGACTACACCTTTCACAGTTATTGGATGCACTGGGTGAAGCAGAGGCTTGGCAAGGC	233	
QY	317	CTAGAGTGGATTCGACCTATTAGTACTATTCTATGGTGTATCCTAGTTTACAACAGAGGTTTC	376	
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QY	377	AAGGGCAAGGCCAATGACTGTAGACAAATCTCTCAACACAGCCTATTTTGGAACTTGCC	436	
Db	298	AAGAGCAAGGCACACTGACTGTAGACAAATCTTCCAGTACAGCCTCATGCAAGCTCAGC	357	
QY	437	AGACTGACACTCTGAGGATTCCTGCCATTATTATTGTGCAAGATCCGATGGTAAATTACGGG	496	
Db	358	AGCCTGACACTCTGAGGACTCTGCGGTCTATTACTGTGCAGACGGTATGGTAACTCTCTTT	417	
QY	497	TATTACTATG-----	506	
Db	418	GACTACTGGGGCCCAAGGAGCACCGGTCAACGCTCTCTCTATAATAAGAGCTATGGGAGCTT	477	
QY	507	-----CTTTTGACTACTCGGGCCAAAGGCACTACGGTCAACGCTCTCTCAGGTGGAGGC	559	
Db	478	GCATGCAAATTCATTTCAAAGGACAGCTCATATATGAATACCTATTGGCTTACGGGACCC	537	
QY	560	GGTTCAGCGCGGAGGTGGCTCTCGCGGTGGCGGA---TCGGATATCGAGCTCACTCAGTCT	616	
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QY	617	CCATCTCTTTGGCTGTCTTAGGGCAGAGGCCACCATATCTCTGAGAGCCAGTGAA	676	
Db	598	CCAGATCTTTGGCTGTCTTAGGGCAGAGGCCACCATATCTCTGAGAGCCAGTGAA	657	
QY	677	AGTGTGTGATAGTTATGGCGTAGTTTTATGCACCTGGTATCAGCAGAAACAGGACAGCCA	736	
Db	658	AGTGTGTGATAGTTATGGCAATAGTTTTATGCAGTGGTACCAGCAGAAACAGGACAGCCA	717	
QY	737	CCAAATCTCTCATCTATCTGTGANTCAAACCTAGAAATCTGGAGTCTCTGCGCAGGTTCAGT	796	
Db	718	CCCAAACTCTCTCATCTATCTGTGATCCAACTTAGAATCTGGGAATCTCTGCCAGGTTCAGT	777	
QY	797	GGCAGTGGGTCTGAGTCAGACTTCACCTCTCACCATCGATCTCTGTGGAGGAAGATGATGCT	856	
Db	778	GGCACTGGGTCTAGGACAGACTTCACCCCTCACCAATTAATCTCTGTGGAGGCTGATGATGTT	837	
QY	857	GCAGTGTATTACTGTCTGCCAAAGATGAGGAAGATCC-----GTACACTTTGGAGGGGGG	910	
Db	838	GCAACTATTATTGTCAACAAGATGATGAGTATCCGTACATGTATCACTTTCGAGGGGGGG	897	

Qy 911 ACCAAGCTCGAAATAAAACGGGGCGCCG 938
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Db 898 ACCAAGCTCGAGATCAAAACGGGGATCCG 925

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Job time : 228 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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 Perfect score: 1030
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length				
1	507.8	49.3	744	21	US-10-879-994-13		Sequence 13, Appl
2	507.8	49.3	744	21	US-10-610-452-13		Sequence 13, Appl
3	505	49.0	1817	21	US-10-489-626-4		Sequence 4, Appl
4	478.6	46.5	717	9	US-09-808-037-5		Sequence 5, Appl
5	478.6	46.5	717	14	US-10-162-889-5		Sequence 5, Appl
6	478.6	46.5	717	17	US-10-384-788-5		Sequence 5, Appl
7	478.6	46.5	717	18	US-10-618-856-5		Sequence 5, Appl

8	478.6	46.5	717	21	US-10-749-522-5	Sequence 5, Appli
9	478.6	46.5	717	24	US-11-073-526-5	Sequence 5, Appli
10	460.4	44.7	1906	21	US-10-491-653-25	Sequence 25, Appli
11	459.8	44.6	756	16	US-10-169-351-68	Sequence 68, Appli
12	447	43.4	1817	21	US-10-489-626-6	Sequence 6, Appli
13	444	43.1	807	16	US-10-408-930-4	Sequence 4, Appli
14	439.4	42.7	783	14	US-10-013-173-36	Sequence 36, Appli
15	439.4	42.7	783	15	US-10-150-762-36	Sequence 36, Appli
16	439.4	42.7	783	13	US-10-244-821-36	Sequence 36, Appli
17	438	42.5	786	19	US-10-689-006-23	Sequence 23, Appli
18	432.4	42.0	809	13	US-10-027-770-1	Sequence 1, Appli
19	431	41.8	726	15	US-10-259-087A-19	Sequence 19, Appli
20	431	41.8	726	9	US-10-689-006-19	Sequence 19, Appli
21	429.4	41.7	729	9	US-09-978-752-10	Sequence 10, Appli
22	423.2	41.1	780	14	US-10-247-488-3	Sequence 3, Appli
23	422	41.0	746	17	US-10-354-246-3	Sequence 3, Appli
24	421.4	40.9	726	15	US-10-259-087A-17	Sequence 17, Appli
25	421.4	40.9	726	19	US-10-689-006-17	Sequence 17, Appli
26	418.8	40.7	879	9	US-09-978-752-22	Sequence 22, Appli
27	417.8	40.6	771	14	US-10-247-488-1	Sequence 1, Appli
28	414.2	40.2	828	18	US-10-257-864A-24	Sequence 24, Appli
29	414.2	40.2	828	20	US-10-645-085A-24	Sequence 24, Appli
30	412.6	40.1	761	17	US-10-354-246-4	Sequence 4, Appli
31	412.6	40.1	828	15	US-10-138-505-31	Sequence 31, Appli
32	412.6	40.1	828	18	US-10-321-131-24	Sequence 24, Appli
33	412.6	40.1	828	18	US-10-399-518-24	Sequence 24, Appli
34	412.6	40.1	828	20	US-10-399-585-24	Sequence 24, Appli
35	409	39.7	5178	21	US-10-688-255-6	Sequence 6, Appli
36	407.6	39.6	1605	18	US-10-257-864A-32	Sequence 32, Appli
37	407.6	39.6	1605	18	US-10-221-131-32	Sequence 32, Appli
38	407.6	39.6	1605	18	US-10-399-518-32	Sequence 32, Appli
39	407.6	39.6	1605	20	US-10-399-585-32	Sequence 32, Appli
40	407.6	39.6	1605	20	US-10-645-085A-32	Sequence 32, Appli
41	406.8	39.5	891	21	US-10-784-305-1	Sequence 1, Appli
42	406.2	39.4	729	17	US-10-354-246-6	Sequence 6, Appli
43	406	39.4	738	21	US-10-861-617-14	Sequence 14, Appli
44	404.6	39.3	828	15	US-10-138-505-25	Sequence 25, Appli
45	404.6	39.3	828	18	US-10-257-864A-20	Sequence 20, Appli

ALIGNMENTS

```

RESULT 1
US-10-879-994-13
; Sequence 13, Application US/10879994
; Publication No. US20050032175A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; APPLICANT: Karrow, Margaret
; APPLICANT: Smith, Eric
; TITLE OF INVENTION: HIGH AFFINITY FUSION
; TITLE OF INVENTION: USE
; FILE REFERENCE: REG 203E2
; CURRENT APPLICATION NUMBER: US/10/879,994
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/610,452
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 744
; TYPE: DNA
; ORGANISM: mus musculus
US-10-879-994-13

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Query Match	49.3%	Score 507.8;	DB 21;	Length 744;
Best Local Similarity	81.8%;	Pred. No. 1.3e-141;		
Matches 613;	Conservative 0;	Mismatches 127;	Indels 9;	Gaps 2;
Qy	186	AGGTCAAGCTGCACGACATCAAGGGGCTGAGCTGTGAGGCGCTTCAGTGAAGATTTT	245	

; TITLE OF INVENTION: DIMERIC AND MULTIMERIC ANTIGEN BINDING STRUCTURE

; FILE REFERENCE: 03528.0142.PCUI00

; CURRENT APPLICATION NUMBER: US/10/489,626

; CURRENT FILING DATE: 2004-03-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4

; LENGTH: 1817

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Plasmid

; US-10-489-626-4

Query Match 49.0%; Score 505; DB 21; Length 1817;

Best Local Similarity 74.3%; Pred. No. 1.3e-140;

Matches 663; Conservative 0; Mismatches 210; Indels 12; Gaps 2;

QY 137 ACCACTGCCGAAGTTTCAGCTGCCGAGCGCCGAGCCGATGCCGAGGTCAAGCTG 196

DB 141 ACGGCAGCGCTGGCTTGCTGCTGGCAGCTCAGCGGCCATGGCGAGGTGCAACTG 200

QY 197 CAGCAGTCAAGGGCTGAGCTGTGAGCCCTGGGGTCTCAGTGAAGATTTCTTCAAGGGT 256

DB 201 CAGCAGTCTGGGGCTGAGCTGTGAGCCCTGGGTCTCAGTGAAGATTTCTTCAAGGGT 260

QY 257 TCTGGCTCACATTTCACTGATTTATGATGATGAGTGGTGAACAGAGTCATGCAAGAGT 316

DB 261 TCTGGCTATGCTAGTACTGATGATGAGTGGTGAACAGAGTGGTGAACAGAGTGGT 320

QY 317 CTAGAGTGAATGGACTTTATAGTACTTACTATGTGATCTTACTATGATCAACAGAGTTTC 376

DB 321 CTTGAGTGGATGGACAGATTTGGCTTGGAGTGGTATGATTAATTAATGGAAGTTTC 380

QY 377 AAGGGCAAGGCCCAATGACTGTAGCAAAATCTTCAACACAGCCATTTTGGAACATTGCC 436

DB 381 AAGGGTAAAGCCACTCTGACTGCAGACGAATCTCCAGCACAGCCATACATGCAACTCAGC 440

QY 437 AGACTGACATCTGAGATTTCTGCCATTTATTTATTTGCAAGATCGATGGTA-----AT 490

DB 441 AGCCTAGCATCTGAGGACTCTGGGTCTATTTCTGTGCAAGCGGAGACTACGACGGTA 500

QY 491 TACGGGTATTAATCTCTTTGGACTACTGGGGCAAGGCACTACGGTCAACCGTCTCTCA 550

DB 501 GGCGGTATTAATCTATGACTACTGGGTCAAGGAACCTCACTACCGTCTCTCA 560

QY 551 G-----GTGGAGCGGTTCAGCGGAGTGGCTCTGGCGGTGGCGGATCGGATATCGAG 604

DB 561 GCCAAACAAACCCCAAGCTTGAAGAAGTGAATTTTCAGAGCACGCGTAGATATCTTG 620

QY 605 CTCACCTAGTCTCCATCTCTTTGGCTGTCTCTAGGGGAGAGGGCCACCATATCTCTGC 664

DB 621 CTCACCAAACTCCAGCTCTTTGGCTGTCTCTAGGGGAGAGGGCCACCATCTCTCTGC 680

QY 665 AGAGCCAGTGAAGTGTGATAGTTATGCGATAGTTTATGCACTGGTATCAGCAGAA 724

DB 681 AAGCCAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740

QY 725 CCAGGACAGCCACCCAACTCTCATCTATCGTGCATCCAACTAGAACTCTGGAGTCCCT 784

DB 741 CCAGGACAGCCACCCAACTCTCATCTATCATGATCCAACTAGTTTCTGGATCCCA 800

QY 785 GCCAGGTTCAGTGGAGTGGTCTGATCAGACTTCACTCTACCATCATCTCTGTTGGAG 844

DB 801 CCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCCACCTCAACATCCATCTCTGGAG 860

QY 845 GAAGATGATGCTGACGTGATTAATCTCTGCAAGATGATGAGATCCGTACAGTTTCGGA 904

DB 861 AAGTGGATGCTGCAACCTATCACTGTAGCAAAAGTACTGAGATCCGTGGAGTTTCGT 920

QY 905 GGGGGACCAAGTGGAAATAAAGCGGGCGGCGCATCGGGTCCGGGGCGGTGGTTCT 964

DB 921 GGAGGACCAAGCTGGAATCAAAAGCGGTGATGCTGCGCGCTGTTGTTCT 980

QY 965 GGTGGTGGTCTCTGGTGGTGGTGGTCTCTGGTGGTGGTGGTCTCTGGC 1009

DB 981 GCGCGCGGTGGTAGCGGTGGTGGCGGCTCCGGTGGTGGTAGC 1025

RESULT 4

US-09-808-037-5

; Sequence 5, Application US/09808037

; Patent No. US20020052311A1

; GENERAL INFORMATION:

; APPLICANT: SOLOMON, Beka

; APPLICANT: HANAN, Bilal

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

; FILE REFERENCE: SOLOMON=2D

; CURRENT APPLICATION NUMBER: US/09/808,037

; CURRENT FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 09/629,971

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 09/473,653

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: US 60/152,417

; PRIOR FILING DATE: 1999-09-03

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 717

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(717)

; US-09-808-037-5

Query Match

Best Local Similarity 46.5%; Score 478.6; DB 9; Length 717;

Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;

QY 186 AGGTCAAGCTCGACAGTCAAGGGCTGAGCTGGTGAAGGCTCGGGTCTCAGTGAAGATTT 245

DB 2 AGGTCAAACTCGAGGAGTCAAGGGCTGAGCTGGTGAAGGCTCGGGTCTCAGTGAAGATTT 61

QY 246 CTGCAAGGGTCTGGCTACATTCACATTCATGATTTAGTATGATGCTGGTGAACAGAGTC 305

DB 62 CTGCAAGGGTCTGGCTACATTCACATTCATGATTTAGTATGATGCTGGTGAACAGAGTC 121

QY 306 ATGCAAAAGAGTCTAGAGTGGATTGGACTTTATTAGTACTTACTATGATGATCTAGTTACA 365

DB 122 ATGCAAAAGAGTCTAGAGTGGATTGGAGTTTATTAGTACTTACTATGATGATCTAGTTACA 181

QY 366 ACCAGAGGTTCAAGGGCAAGGCCACAAATGACTGTAGACAAATCTCTCAACACAGCCTATT 425

DB 182 ACCAGAGGTTCAAGGGCAAGGCCACAAATGACTGTAGACAAATCTCTCAACACAGCCTATA 241

QY 426 TGAACCTGCCAGACTGACATCTGAGGATTCGCCATTTATTATTGTGCAAGATCGGATG 485

DB 242 TGAACCTGCCAGACTGACATCTGAGGATTCGCCATTTATTATTGTGCAAGATCGGATG 301

QY 486 GTAAATTACGGGTATTACTATGCTTTGGACTACTGGGGCCAAAGGCACCTACGGTCACCGTCT 545

DB 302 CTATGTCC-----TACTTTGACTACTGGGGCCAAAGGCACCTACGGTCACCGTCT 349

QY 546 CTTCAAGTGGAGCGGTTCAAGCGGAGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 605

DB 350 CTTCAAGTGGAGCGGTTCAAGCGGAGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC 409

QY 606 TCACCTCAGTCTCCATCTCTTTGGCTGTCTCTAGGCGAGAGGGCCACCATATCTGCA 665

DB 410 TCACCTCAGTCTCCATCTCTTTGGCTGTCTCTAGGCGAGAGGGCCACCATATCTGCA 469

QY 666 GAGCCAGTGAAGTGTGATAGTTTATGCGGATGATTTTATGCACTGGTATGATCAGCAGAAAC 725

Db 470 GTGCCAGCTCAAGTAT-----AAGTTACATGCACCTGGTATCAGCAGAAGC 514
QY 726 CAGGACAGCCACCAACTCCTCATCTATCGTGCATCCCAACTAGAACTCGGAGTCCCTG 785
Db 515 CAGGCACCTCCCCCAAGAGATGGATTATGACACATCCAAACTGGGTTCTGGAGTCCCTG 574
QY 786 CCAAGGTTCAAGTGCAGTGGGTTGAGTCAAGCTTCACTCTCACCATCGATCCTGTGGAGG 845
Db 575 CTCGGTTCAAGTGCAGTGGGTTGAGTCAAGCTTCACTCTCACCATCGATCCTGTGGAGG 634
QY 846 AAGATGATGCTGAGTGTATTAAGTCTGCTGCAAGATGGAAGATCCGTACAGTTCGGAG 905
Db 635 CTGAAGATGCTGCACTTATTAAGTCTGCTGCAAGATGGAAGATCCGTACAGTTCGGAG 694
QY 906 GGGGACCAAGCTGGAATAAAA 928
Db 695 GGGGGCCCAAGCTGGAATAAAA 717
RESULT 5
US-10-162-889-5
; Sequence 5, Application US/10162889
; Publication No. US20030077252A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Bilal
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
; TITLE OF INVENTION: USEFUL IN DIAGNOSING
; FILE REFERENCE: SOLOMON=2B
; CURRENT APPLICATION NUMBER: US/10/162,889
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-162-889-5
Query Match 46.5%; Score 478.6; DB 14; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;
Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;
QY 186 AGGTCAAGCTGCAGCAGTCAAGGGCTGAGTGTGAGGCTGGGGTCTCAGTGAAGATT 245
Db 2 AGGTCAAACTGCAGGAGTCAAGGGCTGAGTGTGAGGCTGGGGTCTCAGTGAAGATT 61
QY 246 CTGCAAGGGTTCTGGCTACACATTCACATGATTATGATGATGCTGGTGAACAGAGTC 305
Db 62 CTGCAAGGGTTCTGGCTACACATTCACATGATTATGATGATGCTGGTGAACAGAGTC 121
QY 306 ATGCAAGAGCTTAGAGTGGATTGGAGTTATTAGTACTTACTATGTTGATCTCTAGTTACA 365
Db 122 ATGCAAGAGCTTAGAGTGGATTGGAGTTATTAGTACTTACTATGTTGATGCTAGTTACA 181
QY 366 ACCAGAGTTCAAGGGCAAGGCCAACATGATCTGTAGCAAACTCTCCAAACAGCCTATT 425
Db 182 ACCAGAGTTCAAGGGCAAGGCCAACATGATCTGTAGCAAACTCTCCAAACAGCCTATA 241
QY 426 TGAACCTTGCAGACTGACATCTGAGGATTCGCCATTTATTATTATGTCAGAGATCGGATG 485
Db 242 TGAACCTTGCAGACTGACATCTGAGGATTCGCCATTTATTATTATGTCAGAGATCGGATG 301

QY 486 GTAATTACGGGTATTACTATATGCTTTGGACTACTGTGGGGCCAAAGCACTACGGTCAACGCTCT 545
Db 302 CTATGTCC-----TACTTTGACTACTGTGGGGCCAAAGTACCAAGGTCAACGCTCT 349
QY 546 CTTCAAGTGGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTTGGCGGATCGGATATCGAGC 605
Db 350 CTTCAAGTGGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTTGGCGGATCGGATATCGAGC 409
QY 606 TCACCTCAGTCTCCATCTCTTTTGGCTGTCTCTTAGGGCAGAGGGCCACATATCTCTGCA 665
Db 410 TCACCTCAGTCTCCAGCAATCATGTCTGCAATCTCCAGGGGAGAGGTCAACATGACCTGCA 469
QY 666 GAGCCAGTGAAGTGTGTATGATGTTATGCGCATGATTTTATGCACTGGTATCAGCAGAAAC 725
Db 470 GTGCCAGCTCAAGTAT-----AAGTTACATGCACCTGGTATCAGCAGAAGC 514
QY 726 CAGGACAGCCACCAAACTCCTCATCTATCGTGCATCCCAACTAGAACTCGGAGTCCCTG 785
Db 515 CAGGCACCTCCCCCAAGAGATGGATTATGACACATCCAAACTGGGTTCTGGAGTCCCTG 574
QY 786 CCAAGGTTCAAGTGCAGTGGGTTGAGTCAAGCTTCACTCTCACCATCGATCCTGTGGAGG 845
Db 575 CTCGGTTCAAGTGCAGTGGGTTGAGTCAAGCTTCACTCTCACCATCGATCCTGTGGAGG 634
QY 846 AAGATGATGCTGAGTGTATTAAGTCTGCTGCAAGATGGAAGATCCGTACAGTTCGGAG 905
Db 635 CTGAAGATGCTGCCACTTATTACTGCCATCAGCGGAGTAGTTACCCATTCACGTTGGAG 694
QY 906 GGGGACCAAGCTGGAATAAAA 928
Db 695 GGGGGCCCAAGCTGGAATAAAA 717
RESULT 6
US-10-384-788-5
; Sequence 5, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON=2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162,889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-384-788-5
Query Match 46.5%; Score 478.6; DB 17; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;

	Matches	597;	Conservative	0;	Mismatches	119;	Indels	27;	Gaps	2;
Qy	186	AGGTCAAGCTGCAGCAGTGCAGGGGCTCAGCTGGTGGAGCCCTGGGGTCTCAGTGAAGATTT	245							
Db	2	AGGTCAAACTGCAGGAGTGCAGGGCTCAGCTGGTGGAGCCCTGGGGTCTCAGTGAAGATTT	61							
Qy	246	CCTGCAAGGGTTCGGGTACACATTCACATTCAGTATGATATGGTATGAGCTGGGTGAAACAGAGTC	305							
Db	62	CCTGCAAGGGTTCGGGTACACATTCACATTCAGTATGATATGCTATGCTGGTGAAGCAGAGTC	121							
Qy	306	ATGCAAAAGAGCTAGAGTGGATTGGACTTATTAGTACTTACTATGGTGTATCCTAGTTTACA	365							
Db	122	ATGCAAAAGAGCTAGAGTGGATTGGAGTTATTAGTACTTACTATGGTGTATCCTAGTTTACA	181							
Qy	366	ACCAGAGTTCAAGGGCAAGGCCCAATAGCTGTAGACAAATCCTCCAAACACAGCCTATT	425							
Db	182	ACCAGAGTTCAAGGGCAAGGCCCAATAGCTGTAGACAAATCCTCCAGCACAGCCTATA	241							
Qy	426	TGGAACTTGCAGAGTACACATCTGAGGATTTCTGCCATTTATTATTGTGCAAGATCGGATG	485							
Db	242	TGGAACTTGCAGAGTACACATCTGAGGATTTCTGCCATTTATTATTGTGCAAGAGGGGCTA	301							
Qy	486	GTAATTACGGGTATTACTATGCTTTTGACTACTGGGGCCAAAGGCACCTACCGTCAACCGTCT	545							
Db	302	CTATGTCC-----TACTTTGACTACTGGGGCCAAAGTGCACACCGTCAACCGTCT	349							
Qy	546	CCTCAGGTGAGGCGGTTTCAGGGCGAGGTGGCTCTTGGCGGTGGCGGATCGGATATCGAGC	605							
Db	350	CCTCAGGTGAGGCGGTTTCAGGGCGAGGTGGCTCTGGCGGTGGCGGATCGGATATCGAGC	409							
Qy	606	TCACTCAGTCTCCATCTTCTTTGGCTGTGCTCTAGGGGAGAGGGCCACCATATCTTGCA	665							
Db	410	TCACTCAGTCTCAGCAATCATGTCTGTCACTCTCCAGGGGAGAAGTCAACATGACCTGCA	469							
Qy	666	GAGCCAGTAAAGTGTGTAGTATTAGCGCATAGTTTTATGCACTGCTATCAGCAGAAAC	725							
Db	470	GTGCCAGCTCAAGTAT-----AGTTACATGCACTGGTATCAGCAGAAGC	514							
Qy	726	CAGGACAGCCACCAAACTCCTCATCTATCGTGCATCCAACTAGAAATCTGGAGTCCCTG	785							
Db	515	CAGGCACCTCCCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTG	574							
Qy	786	CCAGGTTCAGTGGCAGTGGGCTGTAGTGCAGACTTCACTTCACCATCGATCCTGTGGAGG	845							
Db	575	CTCGCTTCAGTGGCAGTGGGCTGTGGGACCTCTTATTCTCTCAAAATCAGCAGCATGGAGG	634							
Qy	846	AAGATGATGCTGCAGTGTATTACTGTCTGCAAAAGTATGGAAGATCCGTACACCGTTCGGAG	905							
Db	635	CTGAAGATGCTGCCACTTATTACTGCCATCAGCGGAGTAGTTACCCATTCACGTTGGAG	694							
Qy	906	GGGGGACCAAGCTGGAAATAAAA	928							
Db	695	GGGGGACCAAGCTGGAAATAAAA	717							

RESULT 7
US-10-618-856-5
; Sequence 5, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: SOLOMON-2A
; CURRENT APPLICATION NUMBER: US/10/618,856
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/473,653A
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5

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; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-618-856-5

Query Match      46.5%; Score 478.6; DB 18; Length 717;
Best Local Similarity 80.3%; Pred. No. 7.7e-133;
Matches 597; Conservative 0; Mismatches 119; Indels 27; Gaps 2;

Qy 186 AGGTCAAGCTGCACAGCTCAGGGGCTCAGCTGTGTGAGGCCCTCGGTGCTCAGTGAAGATTT 245
Db |||||
Qy 2 AGGTCAAACTGCAGGAGTTCAGGGGCTCAGCTGTGTGAGGCCCTCGGTGCTCAGTGAAGATTT 61
Db |||||
Qy 246 CCTCAAGGGTTCCTGGCTACACATTCAGTATGATGATGATGAGCTGGGTGAAACAGAGATC 305
Db |||||
Qy 62 CTGTCAAGGGTTCCTGGCTACACATTCAGTATGATGATGATGAGCTGGGTGAAAGCAGATC 121
Db |||||
Qy 306 ATGCAAAAGAGCTAGAGTGGATTTAGTACTTATTAGTACTTACTATGTGTGATCCTAGTTTACA 365
Db |||||
Qy 122 ATGCAAAAGAGCTAGAGTGGATTTGGAGTATTAGTACTTACTATGTGTGATCCTAGCTTACA 181
Db |||||
Qy 366 ACCAGAGGTTCAAGGGCAAGGCCAATGACTGTGAGCAAAATCCTCCAAACAGAGCCTATT 425
Db |||||
Qy 182 ACCAGAAGTTCAAGGGCAAGGCCAATGACTGTGAGCAAAATCCTCCAGCACAGCCTATA 241
Db |||||
Qy 426 TGGAACTTGCAGACTGACACTCTGAGGATTTCTGCCATTTATTATTGTGCAAGATCGGATG 485
Db |||||
Qy 242 TGGAACTTGCAGACTGACACTCTGAGGATTTCTGCCATTTATTATTGTGCAAGAGGGGCTA 301
Db |||||
Qy 486 GTAATTACGGGTATTACTATGCTTTGGACTACTTGGGGCCAAAGGCACCTACCGTCAACCGTCT 545
Db |||||
Qy 302 CTATGTCC-----TACTTTGACTACTTGGGGCCAAGTCACACCGTCAACCGTCT 349
Db |||||
Qy 546 CCTCAGGTGAGGGGGTTTCAGGGCGAGTGGCTCTTGGCGGTGGCGGATTCGGATATCGAGC 605
Db |||||
Qy 350 CCTCAGGTGAGGGGGTTTCAGGGCGAGTGGCTCTTGGCGGTGGCGGATTCGGATATCGAGC 409
Db |||||
Qy 606 TCACACTGCTCCATCTTCTTTGGCTGTGCTCTTGGGCGAGGGCCACCATATCCTGCA 665
Db |||||
Qy 410 TCACACTGCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACCATGACCTGCA 469
Db |||||
Qy 666 GAGCCAGTGAAGTGTGTGATAGTTATGGCGATAGTTTTATGCACTGGTATCAGCAGAAAC 725
Db |||||
Qy 470 GTGCCAGTCAAGTAT-----AAGTTACATGCATGGTATCAGCAGAAAC 514
Db |||||
Qy 726 CAGGACAGGCCACCAAACTCCTCATCTATCGTGCATCCAAACCTAGAAATCTGGAGTCCCTG 785
Db |||||
Qy 515 CAGGCACTCCCCCAAAGATGGAATTTATGACACATCCAAACTGGGCTTCTGGAGTCCCTG 574
Db |||||
Qy 786 CCAGGTTTCAGTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATCCTGTGGAGG 845
Db |||||
Qy 575 CTGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCAATCAGCAGCATGGAGG 634
Db |||||
Qy 846 AAGATGATGCTGCAGTGTATTACTGTCTGCAAAAGTATGGAAGATCCGATCACGTTGGAG 905
Db |||||
Qy 635 CTGAAGATGCTGCCATTATTACTGCCATCAGCGGAGTAGTTACCCATTACCGTTGGAG 694
Db |||||
Qy 906 GGGGGACCAAGCTGGAAATAAAA 928
Db |||||
Qy 695 GGGGGGCCAAGCTGGAAATAAAA 717

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RESULT 8
US-10-749-522-5
; Sequence 5, Application US/10749522
; Publication No. US20050089510A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: AGENTS AND COM

246	Qy	CCTGCAAGGGTTCTGGCTACACATTCACTGATTAATGGTATGAGCTGGGTGAAACAGAGTC	305
62	Db	CTCTGCGCCCTCTGGATTCACTTTTCAGTAGCTATGGCATGTCTTGGGTTCCGACACTC	121
306	Qy	ATGCAAAAGAGTCTAGAGTGGATTGGACATTTATTAGTACTTACTATGCTGATCCTAGTTACA	365
122	Db	CAGACAGAGGCTGGAGTTGGTTCGCACCAATTAATAGTAATGGTGGTAGCACCCTTTTATC	181
366	Qy	ACCAGAGGTTCAAGGGCAAGGCCCAATGACTGTGTAGACAAATCTCTCCAACACAGCCTATT	425
182	Db	CAGACAGTGTCAAGGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAACAACCTGTACC	241
426	Qy	TGGAACCTGCCAGACTGACATCTCAGGATTCGTGCCATTTATTTATGTCGAGATCGGATG	485
242	Db	TGCAAAATGAGCAGCTCTGAAGTCTCTGAGGACACAGCCATGTATTTACTGTGCAAGAGAAGA	301
486	Qy	GTAATTACGGGTATTACTATATGCT-----TTGGACTCTGGGGCCCAAGGCATACGG	536
302	Db	ATTACCCCTATTACTACGGTAGTAGAGGCTACTTTTGACTCTCTGGGCCCAAGGCCACCG	361
537	Qy	TCACGGTCTCTCAGGTGGAGCGGTTACGGCGGAGGTGGCTCTGGCGGTGGCGGATCGG	596
362	Db	TCACCGTCTCTCAGGTGGAGCGGTTACGGCGGAGGTGGCTCTGGCGGTGGCGGATCGG	421
597	Qy	ATATCGAGCTCACTCAGTCTCCATCTCTCTTTGGCTGTGTCTTAGGGCAGAGGGGCCACCA	656
422	Db	ACATCGAGCTCACTCAGTCTCCAGCTCTCTTTGGCTGTGTCTCTAGGGCAGAGGGGCCACCA	481
657	Qy	TATCCTGCAGAGCCAGTGAAGTGTGTAGTTATGGCGATAGTTTATGCACTCGGTATC	716
482	Db	TATCCTGCAGAGCCAGTGAAGTGTGTAGTTATGGCAATAGTTTATGCACTCGGTATC	541
717	Qy	AGCAGAAACAGGACAGACCCCAAACTCTCATCTATCGTGCATCCAACTCAGTAATCTG	776
542	Db	AGCAGAAACAGGACAGACCCCAAACTCTCATCTATCGTGCATTAATCTAGAAATCTG	601
777	Qy	GAGTCCCTGCAGGTTCAGTGGCAGTGGGTCTGAGTCAGACTTCACTCTCACCATCGATC	836
602	Db	GGATCCCTGCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCCACCTTCAACATTAATC	661
837	Qy	CTGTGGAGGAGATGATCCTCGAGTGTATTAATCTGTCGAAGTATGGAAGATCCGTACA	896
662	Db	CTGTGGAGGCTGATGATGTTGCAACCTATTACTGTACAGAAAGTAATGAGGATCCGTGGA	721
897	Qy	CGTTCCGAGGGGGGACCAAGCTGGAAATAAAACGG	931
722	Db	CGTTCCGTTGAGGACCAACCAAGCTTCGAGATCAAAACGG	756

[illegible]

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RESULT 13
US-10-408-930-4
; Sequence 4, Application US/10408930
; Publication No. US20030170820A1
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION
; FILE REFERENCE: 674537-2003.1
; CURRENT APPLICATION NUMBER: US/10/408,930
; CURRENT FILING DATE: 2003-04-07
; PRIORITY APPLICATION NUMBER: PCT/AU99/00341
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 09/674,677
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: AU P33445

```

```

; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo Sapeins
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(807)
; OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4C2) scFv
US-10-408-930-4

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Query Match	43.1%	Score 444;	DB 16;	Length 807;
Best Local Similarity	76.4%;	Pred. No. 1.9e-122;		
Matches 584;	Conservative 0;	Mismatches 152;	Indels 30;	Gaps 2;

Qy	177	CCATGGCCGAGGCTCAAGCTGCAGCAGATCAGGGGCTGAGCTGGTCAGGCGCTGGGGGCTCTCAG	236
Db	1	CCATGGCCGATGTGAAGCTTCAGAGATCAGGGCTGAGCTGGTCAGGCCCGGGGCTCTCAG	60
Qy	237	TGAAGATTTCTGCAAGGGTTCTGGCTACACATTCACCTGATATTGGTATGAGCTGGGTGA	296
Db	61	TGAAGATTACTGCAAGGGTTCCGGCTACACATTCACCTGATTATGCTATGCTATGGGTGA	120
Qy	297	AACAGAGTCATGCAAGAGATCTAGAGTGGATTGGAGCTATTAGTACTTCTATCGTGTATC	356
Db	121	AGCAGAGTCTATGCCAAGAGTCTAGATGGATTGGAGCTATTAGTAAATTCCTTTGGGTAATA	180
Qy	357	CTAGTTACAACACAGAGGTTCAAGGGCAAGGCCACAATGACATGTAGACAAATTCCTCCAACA	416
Db	181	CAAACTAACACAGAGGTTTGAGGCCAAGGCCACAATGACTGTAGACAAATTCCTCCAACA	240
Qy	417	CAGCCTATTTGGAACTTGCAGACCTGACATCTGAGGATTTGCCATTTATTTATTTGTGCAA	476
Db	241	CAGGCTATTTGGAACTTGGCAGATTGACATCTGAGGATTTCTGCCATCTATTTACTGTGCAA	300
Qy	477	GATCGGATGTTAATACGGGTATTACTATGCTTTGGACTACTGCGGGCCAGGCACTACGG	536
Db	301	GA-----GTGATCGACTGGTCTCTTCGATGTCGCGGCCAAGGGACCAACGG	345
Qy	537	TCACCGTCTCCTCAGGTGGAGGGCGGTTTCAGCGGAGGTGGCTCTGCGGGTGGCGGATCGG	596
Db	346	TCACCGTCTCCTCAGGTGGAGGGCGGTTTCAGCGGAGGTGGCTCTGCGGGTGGCGGATCGG	405
Qy	597	ATATCGAGCTCACTCAGTCTCCATCTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCA	656
Db	406	ACATTTGTGCTGACCCAAATCTCCAGCAATCATGTTTCGCATCTCCAGGGGAGAAGGTCCACCA	465
Qy	657	TATCTCAGAGCCAGTGAAGTCTGTATAGTTATGGCGATAGTTTATGCACTGGGTATC	716
Db	466	TGACCTGCAGTGCCTCACTCAGTGT-----CAGGTACGTGCCTGGTACC	510
Qy	717	AGCAGAAACAGGACAGCCACCCAACTCCTCATCTATCGTGCATCCAACTAGAAATCTG	776
Db	511	AACAGAGTCAGGCACCTCCCCAAAAGATGGAATTTATGACACATTCAAATCGGCTTCTG	570
Qy	777	GAGTCCCTGCCAGGTTTCAGTGGGAGTGGGTCTGAGTCAGACTTCACCTCTCACCATCATC	836
Db	571	GAGTCCCTGCTGCCTTCAGTGGGAGTGGGTCTGGGACCTCTCACTCTCTCTCAAAATCAGCA	630
Qy	837	CTGTGGAGGAAGATGATGCTGCAGTGTATTACTCTGTGCAAGGTATGGAAGATCCGTACA	896
Db	631	GCTTTGGAGGCTGAAGATGCTGCCACTTTATTACTGCCAGCACTGAGGTAGTAAACCTCCCA	690
Qy	897	CGTTTCGAGGGGGGACCAAGCTGGAATAAAACGGGCGGGCGCA	940
Db	691	CGTTTCGCTGTCTGGAGCAAGCTGGAATAAAACGGGCGGGCGCA	734

RESULT 14	US-10-013-173-36	US-10-013-173-36
598	CTCCTCATCTATCGTGCATCCAACCTAGAACTCTGGATCCCTGTCAGTTTCAGTGGCACT	657
Db		
803	GGGTCTGAGTCAGACTTTCACCTCTCACCATCGATCTGTGGAGGAAGATGATGCTGCAGTG	862
QY		

```

; Publication No. US20030095977A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jorh M.
;
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
;
; FILE REFERENCE: 690022.547C1
;
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
;
; NUMBER OF SEQ ID NOS: 69
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 36
;
; LENGTH: 783
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: T84.66 single chain antibody-genomic Streptavidin
; OTHER INFORMATION: fusion construct
;
; US-10-013-173-36

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Query Match	42.7%	Score 439.4	DB 14	Length 783				
Best Local Similarity	76.3%	Pred. No. 4.6e-121						
Matches 599	Conservative 0	Mismatches 141	Indels 45	Gaps 3				
Qy	185	GAGGTC	AAAGCTG	CAGCAGTC	AGGGGCTG	AGCTGGT	GAGCGCTGGGCTCTCAGTGAAGATT	244
Db	1	GAGGTT	CAAGCTG	CAGCAGTC	CGGGG	CAGAGCTTGTG	GAGCCAGGGGCTCAGTCAAGATTG	60
Qy	245	TCCTG	CAAGGGT	TCTGGCT	TACACAT	TCACTGATTAT	TGGTATGAGCTGGGTGAAACAGAGT	304
Db	61	TCCTG	CACAGCT	TCTGGCT	TCAACAT	TAAAGAC	CACTATATGCACCTGGGTGAAGCAGAGG	120
Qy	305	CATG	CAAGAGT	CTAGAGTG	AGTATG	GACTTTAT	TAGTACTTTATCTATGGTGTGATCTCTAGTTTAC	364
Db	121	CCTG	AAACAGGGC	CTGGAATG	GATTGGA	AGGATTTGAT	TCTTCGGAATGGTAAATAGTAAATAT	180
Qy	365	AACCA	GAGGTTCA	AGGGCAAG	GCACAA	TGACTGTAG	ACAAATCCTCCAAACAGAGCTAT	424
Db	181	GTCC	CAAGGTTCA	GGGCAAGG	CCATTA	TAACAGCAG	ACACATCTCTCCAAACAGAGCTTAC	240
Qy	425	TTGGA	ACTTGC	CAGACTG	ACATCTG	AGGATTTCTG	CCATTTATTTGTGCAAGATCGGAT	484
Db	241	CTGCA	GCTCACC	AGCTGAC	ACTGAG	GCACCTG	CCGCTCTATTTATTTGTGC---TTCGGTTT	297
Qy	485	GGTAA	TTACGGG	PATTTACT	ATGCTTT	TGGACTACTGGG	CCAGGCACTACGGTCAACCGTC	544
Db	298	GGTTA	CTAGTG	TCTGACTAT	GTATGG	CCCTACTGGG	GCTCAAGGAACCTCAGTCAACCGTC	357
Qy	545	TCTCA	-----	-----	-----	-----	GGTGGAGCGGTTCA	565
Db	358	TCCTC	AAAGATCT	CTGGTGG	CGGTGG	CTCGGGG	TGTGGGTGGCGCGGCTCG	417
Qy	566	GGCGG	AGGTGG	CTCTGG	CGGTGG	CGGATCG	---GATATCGAGCTCACTCAGTCTCCATCT	622
Db	418	GGTGG	TGGTGGG	TGCGGCG	CGCGCT	CGAGCG	ACATTTGCTGTGACCCAAATCTCCAGCT	477
Qy	623	TC	TTTGGCTGT	GTCTTAG	GGGCGAG	GGGCCAC	CAATATCTGTGAGAGCCAGTGAAGTGT	682
Db	478	TC	TTTGGCTGT	GTCTTGGG	CAGAGGG	CCACTAT	GTCTGTGAGAGCCGTGAAAGTGT	537
Qy	683	GATAG	TATGGCG	ATAGTTTT	TATGCA	CTGGTATC	AGCAAAACCCAGGACGCCACCCAA	742
Db	538	GATAT	TTTTTGGG	CGTGGG	TTTTTGG	CACTGGT	ACCAGCAAAACCCAGGACGCCACCCAA	597
Qy	743	CTCCT	CATCTAT	CTCGTGC	ATCCAA	CTCTAG	AGTCTCGGAGTCCCTGCGCAGGTTTCAGTGGCAGT	802
Db	598	CTCCT	CATCTAT	CTCGTGC	ATCCAA	CTCTAG	AGTCTCGGAGTCCCTGCGCAGGTTTCAGTGGCAGT	557
Qy	803	GGG	CTGAGT	TCAGCTT	CACTCT	CAACCAT	TCGATCTCTGTGGAGGAAGATGATGCTGCAGTG	862

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 1533 Seconds
(without alignments)
83.003 Million cell updates/sec

Title: US-10-089-278-6
Perfect score: 1725
Sequence: 1 MDCLTLNLSAEGKVDQASKI.....GSGGGSGGGSGSPVQFI 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1725	100.0	329	4 AAB70840	Aab70840 SNV-env 1
2	1239	71.8	330	4 AAB70842	Aab70842 SNV-env 1
3	1202.5	69.7	335	4 AAB70843	Aab70843 SNV-env 1
4	1186.5	68.8	309	4 AAB70841	Aab70841 SNV-env 1
5	1098	63.7	291	6 ABR42054	Abr42054 Newcasttle
6	1045.5	60.6	543	7 ADD12876	Add12876 CD28/mela
7	1004	58.2	302	4 AAB70844	Aab70844 SNV-env 1
8	993.5	57.6	729	4 AAB20439	Aab20439 Antibody
9	992.5	57.5	231	4 AAB20443	Aab20443 Antibody
10	992.5	57.5	322	4 AAB20440	Aab20440 Antibody
11	991	57.4	298	8 ADS88777	Ads88777 Amino aci
12	991	57.4	554	3 AAY50822	Aay50822 Fv-antibo
13	983	57.0	305	3 AAY51142	Aay51142 Murine de
14	983	57.0	305	3 AAY59265	Aay59265 Antibody
15	978	56.7	260	2 AAW95600	Aaw95600 Anti-digo
16	978	56.7	260	2 AAW89101	Aaw89101 Anti-digo
17	974.5	56.5	562	6 ABR57059	Abr57059 Plasmid p
18	948.5	55.0	500	7 ADD13792	Add13792 Plasmid p
19	947.5	54.9	252	4 AAU07497	Aau07497 Synthetic
20	946.5	54.9	271	2 AAW02293	Aaw02293 FvKC-II-K
21	935.5	54.2	239	4 AAB47111	Aab47111 scfv 508F
22	935.5	54.2	239	6 AAO16066	Aao16066 Human neu
23	935.5	54.2	239	6 ADJ88113	Adj88113 Human bet
24	927	53.7	261	8 ADT91213	Adt91213 Single ch
25	924	53.6	331	6 AAE37727	Aae37727 Chemokine

ALIGNMENTS

RESULT 1

AAB70840
ID AAB70840 standard; protein; 329 AA.

XX AC AAB70840;

XX DT 11-SEP-2003 (revised)

XX DT 25-JUN-2001 (first entry)

XX DE SNV-env leader/human 7A5-scFv fusion construct.

XX KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.

XX OS Homo sapiens.

XX OS Spleen necrosis virus.

XX OS Chimeric.

Key	Location/Qualifiers
FT Protein	1..45
FT Protein	/label= SNV-env_leader
FT Protein	46..329
FT Protein	/label= 7A5-scFv

DE19946142-A1.

PD 29-MAR-2001.

PF 27-SEP-1999; 99DE-01046142.

PR 27-SEP-1999; 99DE-01046142.

XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.

PI Cichutek K, Engelstaedter M;

XX WPI; 2001-246140/26.

DR N-PSDB; AAF61509.

XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy of e.g. acquired immune deficiency syndrome, encodes a single-chain variable antibody fragment.

XX Claim 1; Fig 1; 18pp; German.

XX

This invention describes a novel cell-targeting vector (A) containing a DNA sequence (I) encoding a single-chain variable antibody fragment (scFv). The products of the invention have antiviral, cytostatic and immunostimulant activity and can be used in gene therapy, immunization and diagnosis particularly of T cell-associated diseases, specifically acquired immune deficiency syndrome (AIDS), severe combined immune deficiency (SCID) or T cell lymphoma. (A) target T cells, independently of the CD4 receptor, with high selectivity, 4-5 fold selectivity over human B cells, and 1000 fold selectivity over other human cells. A vector designated 7A5 encodes a 329 amino acid single-chain variable antibody fragment, fully defined in the specification. It was used to transform D17 (canine osteosarcoma cells susceptible to spleen necrosis virus (SNV)) cells, C8166 (human T lymphocyte) cells, and Hela (human cervical carcinoma) cells. After 48 hours, the cells were stained with X-gal to determine transfection. The viral titer (infectious units/ml) was over 1 million for D17, 1 million for C8166 but less than 100 for Hela, showing the high selectivity for human T cells. This sequence represents the SNV-env leader/human 7A5-scFv fusion construct used in the construction of novel cell targeting vectors described in the invention. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 329 AA:

Key	Location/Qualifiers
Protein	1. .45
FT	/label= SNV-env_leader
FT	46. .330
FT	/label= 7B2-scFv
XX	
FN	DE19946142-A1.
XX	
PD	29-MAR-2001.
XX	
PF	27-SEP-1999; 99DE-01046142.
XX	
PR	27-SEP-1999; 99DE-01046142.
XX	
PA	(BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.
XX	
PI	Cichutek K, Engelstaedter M;
XX	
WP1	2001-246140/26.
DR	N-PSDB; AAF61511.
DR	
XX	
PT	Cell-targeting vector selective for T lymphocytes, useful in gene therapy
FT	of e.g. acquired immune deficiency syndrome, encodes a single-chain
FT	variable antibody fragment.
XX	
PS	Claim 1; Fig 3; 18pp; German.
XX	
CC	This invention describes a novel cell-targeting vector (A) containing a
CC	DNA sequence (I) encoding a single-chain variable antibody fragment
CC	(scFv). The products of the invention have antiviral, cytostatic and
CC	immunostimulant activity and can be used in gene therapy, immunization
CC	and diagnosis particularly of T cell-associated diseases, specifically
CC	acquired immune deficiency syndrome (AIDS), severe combined immune
CC	deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC	of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC	human B cells, and 1000 fold selectivity over other human cells. A vector
CC	designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC	fragment, fully defined in the specification. It was used to transform
CC	D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC	(SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC	carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC	determine transformation. The viral titer (infectious units/ml) was over
CC	1 million for D17, 1 million for C8166 but less than 100 for HeLa,
CC	showing the high selectivity for human T cells. This sequence represents
CC	the SNV-env leader/human 7B2-scFv fusion construct used in the
CC	construction of novel cell targeting vectors described in the invention.
CC	(Updated on 11-SEP-2003 to standardise OS field)
XX	
SO	Sequence 330 AA:

[illegible]

CC (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 315 AA;

Query Match 69.7%; Score 1202.5; DB 4; Length 315;
Best Local Similarity 73.8%; Pred. No. 1.3e-65;
Matches 236; Conservative 30; Mismatches 47; Indels 7; Gaps 4

QY 1 MDCLTNLRSABGKVDQASKILILLVAMWGFGTTAEVSTARRAAQPMAYEYKLOQSGAELVR 60
DB 1 MDCLTNLRSABGKVDQASKILILLVAMWGFGTTAEVSTARRAAQPMAYEYKLOQSGAELVR 60

QY 61 PGVSVKISCKSGYFTFDYMSWVQSHAKSLEWIGLISLTYGDPDSYNQRFKGMATMTVD 120
DB 61 PGASVVKISCKSGYFTFDYMSWVQSHAKSLEWIGLISLTYGDPDSYNQRFKGMATMTVD 120

QY 121 KSNATYELARLTSEDSAIYYCARS-DGNYGVYALDYWGOGTTVTYSSGGSGGGGGS 179
DB 121 KSNATYELARLTSEDSAIYYCARS-DGNYGVYALDYWGOGTTVTYSSGGSGGGGGS 179

QY 180 GGGGSDIELTQSPSSLAIVSLQRTATISCRASESDVSDGSMHWYQKPGPPKLLIYRA 239
DB 179 GGGGSDIELTQSPSSLAIVSLQRTATISCRASESDVSDGSMHWYQKPGPPKLLIYRT 235

QY 240 SNLESGVPARFSGSGSESDFTLTIDPVEDDAVYVCIQSMEDEPTVFGGKLEIKRAAA 299
DB 236 SNLACGVPARFSGSGSGTSYSLTIGTMEAEADVATYCCQSGSIPYTFGGGTKEIKRAAA 295

QY 300 SGSGGGGS-GGGSGGGSGG 318
DB 296 SGSGGGGGGGGGSGGGGGG 315

RESULT 4

AAB70841

ID AAB70841 standard; protein; 309 AA.

XX
AC AAB70841;

XX
DT 11-SEP-2003 (revised)

XX
DT 25-JUN-2001 (first entry)

XX
DE SNV-env leader/human K6-scFv fusion construct.

XX
KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.

XX
OS Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX
FH Key Location/Qualifiers

FT Protein 1..45 /label= SNV-env_leader

FT Protein 46..315 /label= K6-scFv

FT

XX
DE19946142-A1.

XX
29-MAR-2001.

XX
27-SEP-1999; 99DE-01046142.

XX
27-SEP-1999; 99DE-01046142.

XX
(BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.

XX
Cichutek K, Engelstaedter M;

XX
WPI; 2001-246140/26.

XX
N-PSDB; AAP61512.

XX
Cell-targeting vector selective for T lymphocytes, useful in gene therapy
of e.g. acquired immune deficiency syndrome, encodes a single-chain
variable antibody fragment.

XX
Claim 1; Fig 4; 18pp; German.

XX
This invention describes a novel cell-targeting vector (A) containing a
DNA sequence (I) encoding a single-chain variable antibody fragment
(scFv). The products of the invention have antiviral, cytostatic and
immunostimulant activity and can be used in gene therapy, immunization
and diagnosis particularly of T cell-associated diseases, specifically
acquired immune deficiency syndrome (AIDS), severe combined immune
deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
human B cells, and 1000 fold selectivity over other human cells. A vector
designated 7A5 encodes a 329 amino acid single-chain variable antibody
fragment, fully defined in the specification. It was used to transform
D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
(SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
carcinoma) cells. After 48 hours, the cells were stained with X-gal to
determine transfection. The viral titer (infectious units/ml) was over
1 million for D17, 1 million for C8166 but less than 100 for HeLa,
showing the high selectivity for human T cells. This sequence represents
the SNV-env leader/human 7E4-scFv fusion construct used in the
construction of novel cell targeting vectors described in the invention.

CC (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 315 AA;

Query Match 69.7%; Score 1202.5; DB 4; Length 315;
Best Local Similarity 73.8%; Pred. No. 1.3e-65;
Matches 236; Conservative 30; Mismatches 47; Indels 7; Gaps 4

QY 1 MDCLTNLRSABGKVDQASKILILLVAMWGFGTTAEVSTARRAAQPMAYEYKLOQSGAELVR 60
DB 1 MDCLTNLRSABGKVDQASKILILLVAMWGFGTTAEVSTARRAAQPMAYEYKLOQSGAELVR 60

QY 61 PGVSVKISCKSGYFTFDYMSWVQSHAKSLEWIGLISLTYGDPDSYNQRFKGMATMTVD 120
DB 61 PGASVVKISCKSGYFTFDYMSWVQSHAKSLEWIGLISLTYGDPDSYNQRFKGMATMTVD 120

QY 121 KSNATYELARLTSEDSAIYYCARS-DGNYGVYALDYWGOGTTVTYSSGGSGGGGGS 179
DB 121 KSNATYELARLTSEDSAIYYCARS-DGNYGVYALDYWGOGTTVTYSSGGSGGGGGS 179

QY 180 GGGGSDIELTQSPSSLAIVSLQRATISCRASESDVSDGSMFHWYQKPGPPKLLIYRA 239
DB 179 GGGGSDIELTQSPSSLAIVSLQRATISCRASESDVSDGSMFHWYQKPGPPKLLIYRT 235

QY 240 SNLESGVPARFSGSGSESDFTLTIDPVEDDAVYVCIQSMEDEPTVFGGKLEIKRAAA 299
DB 236 SNLACGVPARFSGSGSGTSLTIGTMEAEADVATYCCQSGSIPYTFGGGTKEIKRAAA 295

QY 300 SGSGGGGS-GGGSGGGSGG 318
DB 296 SGSGGGGGSGGGSGGGSGG 315

RESULT 4

AAB70841

ID AAB70841 standard; protein; 309 AA.

XX
AC AAB70841;

XX
DT 11-SEP-2003 (revised)

XX
DT 25-JUN-2001 (first entry)

XX
DE SNV-env leader/human K6-scFv fusion construct.

XX
KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.

XX
OS Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX
FH Key Location/Qualifiers

FT Protein 1..45 /label= SNV-env_leader

FT Protein 46..315 /label= K6-scFv

XX
DE19946142-A1.

XX
29-MAR-2001.

XX
27-SEP-1999; 99DE-01046142.

XX
27-SEP-1999; 99DE-01046142.

XX
(BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.

XX
Cichutek K, Engelstaedter M;

XX
WPI; 2001-246140/26.

XX
N-PSDB; AAP61512.

XX
Cell-targeting vector selective for T lymphocytes, useful in gene therapy
of e.g. acquired immune deficiency syndrome, encodes a single-chain
variable antibody fragment.

XX
Claim 1; Fig 4; 18pp; German.

XX
This invention describes a novel cell-targeting vector (A) containing a
DNA sequence (I) encoding a single-chain variable antibody fragment
(scFv). The products of the invention have antiviral, cytostatic and
immunostimulant activity and can be used in gene therapy, immunization
and diagnosis particularly of T cell-associated diseases, specifically
acquired immune deficiency syndrome (AIDS), severe combined immune
deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
human B cells, and 1000 fold selectivity over other human cells. A vector
designated 7A5 encodes a 329 amino acid single-chain variable antibody
fragment, fully defined in the specification. It was used to transform
D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
(SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
carcinoma) cells. After 48 hours, the cells were stained with X-gal to
determine transfection. The viral titer (infectious units/ml) was over
1 million for D17, 1 million for C8166 but less than 100 for HeLa,
showing the high selectivity for human T cells. This sequence represents
the SNV-env leader/human 7E4-scFv fusion construct used in the
construction of novel cell targeting vectors described in the invention.

DR	N-PSDB; AAF61510.	OS	Mus sp.
XX		XX	
PT	Cell-targeting vector selective for T lymphocytes, useful in gene therapy	FT	Key Location/Qualifiers
PT	of e.g. acquired immune deficiency syndrome, encodes a single-chain	FT	Misc-difference 2 /note= "Encoded by AAAQ"
PT	variable antibody fragment.	FT	Misc-difference 274. .277
XX		FT	Misc-difference /note= "Encoded by GCAGGA"
PS	Claim 1; Fig 2; 18pp; German.	XX	
CC	This invention describes a novel cell-targeting vector (A) containing a	PN	EP1275724-A1.
CC	DNA sequence (I) encoding a single-chain variable antibody fragment	XX	
CC	(scFv). The products of the invention have antiviral, cytostatic and	PD	15-JAN-2003.
CC	immunostimulant activity and can be used in gene therapy, immunization	XX	
CC	and diagnosis particularly of T cell-associated diseases, specifically	PF	10-JUL-2001; 2001EP-00116847.
CC	acquired immune deficiency syndrome (AIDS), severe combined immune	XX	
CC	deficiency (SCID) or T cell lymphoma. (A) target T cells, independently	PR	10-JUL-2001; 2001EP-00116847.
CC	of the CD4 receptor, with high selectivity, 4-5 fold selectivity over	XX	
CC	human B cells, and 1000 fold selectivity over other human cells. A vector	PA	(SCHL/) SCHIRRMACHER V.
CC	designated 7A5 encodes a 329 amino acid single-chain variable antibody	XX	
CC	fragment, fully defined in the specification. It was used to transform	PI	Schirmacher V;
CC	DI7 (canine osteosarcoma cells susceptible to spleen necrosis virus	DR	WPI; 2003-315856/31.
CC	(SNV)) cells. C8166 (human T lymphocyte) cells, and HeLa (human cervical	DR	N-PSDB; ACC57513.
CC	carcinoma) cells. After 48 hours, the cells were stained with X-gal to	XX	
CC	determine transformation. The viral titer (infectious units/ml) was over	XX	
CC	1 million for DI7, 1 million for C8166 but less than 100 for HeLa,	PT	Bonding reagent for costimulating effector cell, comprises two portions
CC	showing the high selectivity for human T cells. This sequence represents	PT	with peptide sequences for single chain Fv fragments directed against
CC	the SNV-env leader/human K6-scFv fusion construct used in the	PT	cell surface protein and costimulatory acting molecule of effector cell.
CC	construction of novel cell targeting vectors described in the invention.	XX	
CC	(Updated on 11-SEP-2003 to standardise OS field)	XX	
XX		PS	Claim 2; Fig 7b; 30pp; English.
SQ	Sequence 309 AA;	XX	
Query Match	68.8%; Score 1186.5; DB 4; Length 309;		
Best Local Similarity	71.6%; Pred. No. 1.2e-64;		
Matches 229; Conservative	26; Mismatches 54; Indels 11; Gaps 2;		
Qy	1 MDCLTNLSRAGKVDQASKILILLVAMWGFQTTAEVSTARAQAQMAAEVKLOQSGAELVR 60		
Db	1 MDCLTNLSRAGKVDQASKILILLVAMWGFQTTAEVSTARAQAQMAAEVKLOQSGTELVK 60		
Qy	61 PGVSVKISCKSGYTFDYDGMVVKQSHAKSLWIGLITSTYDPSYNQRFKATMTVD 120		
Db	61 PGASVNLSCASGYTFSTYVHMLKQRPQGLEWIGEIDPVDSTYTNQNFKQKATLTVD 120		
Qy	121 KSNNTAYLELARTSDESAIYCARSDNGYGYVYALDYWGQGTVTYVSSGGSGGGGG 180		
Db	121 KSTTYVHMLSSLTSDSAVYICARG- ----YAMDYWGQGTNTVTVSSGCGSGGGGG 174		
Qy	181 GCGSDIELTQPSLAVSLGQRTATISCRASESDSYGDSFMHWYQKPGPPKLLIYRAS 240		
Db	175 GCGSDIELTQSPAIMSASPGKVTWTCASSI- ----SYMHWYQKPGTSPKRWIYDTS 229		
Qy	241 NLESGVPARFSGSGESDFTLTIDPVEEDAAVYICLQSMEDPVTFGGKLEIKRAAAS 300		
Db	230 KLASGVPAARESGSGTSYSLPISSEAEADAATYICHRSSYPWTFGGKLEIKRAAAS 289		
Qy	301 GSGGGSGGGSGGGGGGG 320		
Db	290 GSGGGSGGGSGGGGGGG 309		
RESULT 5			
ABR42054			
ID	ABR42054	standard; protein; 291 AA.	
XX			
AC	ABR42054;		
XX			
DT	11-AUG-2003 (first entry)		
XX			
DE	Newcastle disease virus F protein scFv.		
XX			
KW	Newcastle disease virus; NDV; F protein; scFv; antibody; vaccine; tumour;		
KW	antitumour; mouse.		
XX			

OS	Mus sp.	XX	
XX		XX	
FT	Key Location/Qualifiers	FT	Misc-difference 2 /note= "Encoded by AAAQ"
FT	Misc-difference 274. .277	FT	Misc-difference /note= "Encoded by GCAGGA"
XX		XX	
PN	EP1275724-A1.	XX	
XX		PD	15-JAN-2003.
XX		XX	
PF	10-JUL-2001; 2001EP-00116847.	XX	
XX		PR	10-JUL-2001; 2001EP-00116847.
XX		XX	
PA	(SCHL/) SCHIRRMACHER V.	XX	
XX		PI	Schirmacher V;
XX		DR	WPI; 2003-315856/31.
XX		DR	N-PSDB; ACC57513.
XX		XX	
PT	Bonding reagent for costimulating effector cell, comprises two portions	XX	
PT	with peptide sequences for single chain Fv fragments directed against	XX	
PT	cell surface protein and costimulatory acting molecule of effector cell.	XX	
XX		PS	Claim 2; Fig 7b; 30pp; English.
XX		XX	
CC	The present sequence is the protein sequence of a single chain Fv	CC	
CC	fragment (scFv) directed against the F protein of Newcastle disease virus	CC	
CC	(NDV) on the cell surface of NDV infected cells. The scFv was derived	CC	
CC	from an NDV-immunised mouse. The invention provides a claimed bonding	CC	
CC	reagent for costimulating an effector cell. The bonding reagent comprises	CC	
CC	an scFv (such as the present NDV(F) scFv) directed against a cell surface	CC	
CC	protein and an scFv directed against a costimulatory acting molecule such	CC	
CC	as CD2, CD3, CD20, CD22, CD26, CD28 or CTLA-4 receptor. Expression	CC	
CC	plasmids comprising DNA encoding the bonding reagent are claimed. A	CC	
CC	vaccine having inactivated cells is also claimed, in which one or more	CC	
CC	bonding reagents are bound to a cell surface protein. Such a vaccine	CC	
CC	preferably includes tumour cells. A pharmaceutical composition comprising	CC	
CC	a bonding reagent is suitable for treating tumours in a subject. In a	CC	
CC	preferred embodiment, the subject is first treated with a tumour-specific	CC	
CC	NDV virus under conditions that allow the cells of the tumour to be	CC	
CC	infected by the virus and express virally encoded proteins. A bonding	CC	
CC	reagent of the invention comprising a binding domain specific for an NDV	CC	
CC	protein expressed on the surface of the tumour cells is then administered	CC	
XX		XX	
SQ	Sequence 291 AA;	XX	
Query Match	63.7%; Score 1098; DB 6; Length 291;		
Best Local Similarity	80.1%; Pred. No. 2.7e-59;		
Matches 209; Conservative	24; Mismatches 26; Indels 2; Gaps 1;		
Qy	41 AAQAPAAEVKIQSGAELVRPGVSVKISCKSGYTFDYDGMVVKQSHAKSLWIGLIT 100		
Db	16 AAQAPAAQVQIQSGPELVKPGASVKISCKTSGYTFADYYMNVKQSHGKLTLEWGLNP 75		
Qy	101 YYGDPSSYNQRFKATMTVDKSSNTAYLELARTLSDESAIYCARSDNGY- -GYVYALDY 158		
Db	76 TNGGTTYNQKFKGATMTVDKSSSTAYMELSLTSDSAVYICARGAYTYDNGPYVAMDY 135		
Qy	159 WQGGTTVTVSSGGSGGGGGSDIELTQSPSLAVSLGQRTATISCRASESDSYGVD 218		
Db	136 WQGGTTVTVSSGGSGGGGGSDIELTQSPASLAVSLGQRTATISCRASESDSYGYN 195		
Qy	219 SFMHWYQKPGPPKLLIYRASNLGSGVPARFSGSGESDFTLTIDPVEEDAAVYICLQ 278		
Db	196 SFIIHWFQKPGPPKLLIFRASNLGSGIPARFSGSGSRDFTLTINPVEADDAATYFCQ 255		
Qy	279 SMEDPYTGGGKLEIKRAAA 299		
Db	256 TNEEDRTTGGGKLEIKRAAA 276		

Query Match	63.7%; Score 1098; DB 6; Length 291;		
Best Local Similarity	80.1%; Pred. No. 2.7e-59;		
Matches 209; Conservative	24; Mismatches 26; Indels 2; Gaps 1;		
Qy	41 AAQPAMAEVKLOQSGAELVRPGVSVKISCKSGYTFDYDGMVVKQSHAKSLWIGLIS 100		
Db	16 AAQPAMAEVKLOQSGAELVRPGVSVKISCKSGYTFDYDGMVVKQSHAKSLWIGLIS 75		
Qy	101 YYGDPSPYNQRFKATMTVDKSNNTAYLELARTSDESAIYCARSDNGY- -GYVYALDY 158		
Db	76 TNGGTTYNQRFKATMTVDKSNNTAYLELARTSDESAIYCARSDNGY- -GYVYALDY 135		
Qy	159 WGQGTVTYVSSGGSGGG 218		
Db	136 WGQGTVTYVSSGGSGGG 195		
Qy	219 SFMHWYQKPGPPKLLIYRASNLGSGVPAARESGSGESDFTLTIDPVEEDAAVYICLQ 278		
Db	196 SFTHWFQKPGPPKLLIYRASNLGSGVPAARESGSGESDFTLTIDPVEEDAAVYICLQ 255		
Qy	279 SMEDPYTFGGGKLEIKRAAA 299		
Db	256 TNEDPRTFGGKLEIKRAAA 276		
XX			
SQ	Sequence 291 AA;		

The present sequence is the protein sequence of a single chain Fv fragment (scFv) directed against the F protein of Newcastle disease virus (NDV) on the cell surface of NDV infected cells. The scFv was derived from an NDV-immunised mouse. The invention provides a claimed bonding reagent for costimulating an effector cell. The bonding reagent comprises an scFv (such as the present NDV(F) scFv) directed against a cell surface protein and an scFv directed against a costimulatory acting molecule such as CD2, CD3, CD19, CD20, CD22, CD26 or CTLA-4 receptor. Expression plasmids comprising DNA encoding the bonding reagent are claimed. A vaccine having inactivated cells is also claimed, in which one or more bonding reagents are bound to a cell surface protein. Such a vaccine preferably includes tumour cells. A pharmaceutical composition comprising a bonding reagent is suitable for treating tumours in a subject. In a preferred embodiment, the subject is first treated with a tumour-specific NDV virus under conditions that allow the cells of the tumour to be infected by the virus and express virally encoded proteins. A bonding reagent of the invention comprising a binding domain specific for an NDV protein expressed on the surface of the tumour cells is then administered

Bonding reagent for costimulating effector cell, comprises two portions with peptide sequences for single chain Fv fragments directed against cell surface protein and costimulatory acting molecule of effector cell.

Claim 2; Fig 7b; 30pp; English.

The present sequence is the protein sequence of a single chain Fv fragment (scFv) directed against the F protein of Newcastle disease virus (NDV) on the cell surface of NDV infected cells. The scFv was derived from an NDV-immunised mouse. The invention provides a claimed bonding reagent for costimulating an effector cell. The bonding reagent comprises an scFv (such as the present NDV(F) scFv) directed against a cell surface protein and an scFv directed against a costimulatory acting molecule such as CD2, CD3, CD19, CD20, CD22, CD26 or CTLA-4 receptor. Expression plasmids comprising DNA encoding the bonding reagent are claimed. A vaccine having inactivated cells is also claimed, in which one or more bonding reagents are bound to a cell surface protein. Such a vaccine preferably includes tumour cells. A pharmaceutical composition comprising a bonding reagent is suitable for treating tumours in a subject. In a preferred embodiment, the subject is first treated with a tumour-specific NDV virus under conditions that allow the cells of the tumour to be infected by the virus and express virally encoded proteins. A bonding reagent of the invention comprising a binding domain specific for an NDV protein expressed on the surface of the tumour cells is then administered

CC activated T cells is required, so proliferation of T cells is not
CC limited. The antibodies of the invention are useful for treating cells to
CC effect supra-agonistic tumour cell-induced activation of T cells such
CC that no additional exogenous stimulus is required. The antibodies are
CC cytostatic and are useful for the treatment and prevention of tumours.
CC This sequence represents the bispecific antibody constructed from CD28
CC and a melanoma-associated proteoglycan.
XX
SQ Sequence 543 AA;

Query Match 60.6%; Score 1045.5; DB 7; Length 543;
Best Local Similarity 72.2%; Pred. No. 7.7e-56;
Matches 205; Conservative 25; Mismatches 41; Indels 13; Gaps 3;

Qy 27 WMGFGTTAEVSTARAQAAM-----AEYKLOQSGAELVPGVSVKISKSGGYTF 76
Db 256 YMGQGTITVTSSASTKGPSVFLAPSSSGSGQVKLQSGPELVKPGASVKISKASGYAF 315

Qy 77 TDYGMVMVKQSHAKSLEWIGLSTYYGDPYSYNORFKGKATMTVDKSNNTAYLELRLTSE 136
Db 316 SRSMNMVVKRPGQGLEWIGRIYPGDGTNYNGKFKGKATLTADKSSSTAYMQVSSLTSV 375

Qy 137 DSAIYYCARSDGNYGY-YALDYWGQGTITVTSSSGGGGGGGGGGGGGGGGGGGGGGGGGSSSL 195
Db 376 DSAVYFCAR--GNTVVVPYTM DYWGQGTITVTSSSGGGGGGGGGGGGGGGGGGGGGGGGGSSSL 433

Qy 196 AVSLGQRATISCRASESDSYGDSFMHWYQKPGQPPLLIYPASNLGSGVPAFSGSGS 255
Db 434 AVSLGQRATISCRASESDSYGDSFMHWYQKPGQPPLLIYPASNLGSGVPAFSGSGS 493

Qy 256 ESDFTLTIDPVEDDAAYVYCLOSMEDPYTFGGGTTKLEIKRAAA 299
Db 494 RTDFTLTIDPVEDDAAYVYCQNNEDPLTFGGGTTKLEIKRAAA 537

RESULT 7
AAB70844
ID AAB70844 standard; protein; 302 AA.
XX
AC AAB70844;
XX
DT 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry)
XX
DE SNV-env leader/human 6C3-scFv fusion construct.
XX
KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct.
XX
OS Homo sapiens.
OS Spleen necrosis virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Protein 1..45
FT Protein /label= SNV-env_leader
FT Protein 46..302
FT Protein /label= 6C3-scFv
XX
PN DE19946142-A1.
XX
XX 29-MAR-2001.
XX
PF 27-SEP-1999; 99DE-01046142.
XX
PR 27-SEP-1999; 99DE-01046142.
XX
PA (BUND) BUNDESREPUBLIK DEUT PAUL-BEHLICH-INST.
XX
PI Cichutek K, Engelstaedter M;

RESULT 6
ADD12876
ID ADD12876 standard; protein; 543 AA.
XX
AC ADD12876;
XX
DT 01-JAN-2004 (first entry)
XX
DE CD28/melanoma-associated proteoglycan bispecific antibody.
XX
KW antibody; bispecific; VH chain; VL chain; T cell receptor; CD28;
KW tumour antigen; variable domain; light chain; heavy chain; heavy domain;
KW single-chain Fv antibody; scFv; melanoma-associated proteoglycan;
KW HER-2/neu; CD20; T cell activation; cytostatic; tumour.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 21..132
FT Region /note= "VL 9.3 (CD28 derived fragment)"
FT Region 133..147
FT Region /note= "FL region"
FT Region 148..267
FT Region /note= "VH 9.3 (CD28 derived fragment)"
FT Region 268..286
FT Region /note= "L region"
FT Region 287..407
FT Region /note= "VH 9.2.27 (melanoma-associated proteoglycan
FT Region 408..422 derived fragment)"
FT Region /note= "FL region"
FT Region 423..543
FT Region /note= "VL 9.2.27 (melanoma-associated proteoglycan
FT Region associated fragment)"
XX
WO2003042231-A2.
XX
XX 22-MAY-2003.
XX
XX 09-NOV-2002; 2002WO-EP012545.
XX
PR 12-NOV-2001; 2001DE-01056482.
XX
XX (JUNG/) JUNG G.
XX (JUNG/) JUNG G.
XX
XX Jung G, Jung G;
XX
XX WPI; 2003-457489/43.
XX
XX New bispecific antibody, useful for inducing T cell mediated destruction
XX of tumor cells, has binding sites for tumor antigen and CD28 T cell
XX receptor.
XX
XX Example 1; Fig 1b; 33pp; German.
XX
XX This invention describes a novel bispecific antibody comprising one
XX binding site for the T cell receptor CD28 and a second for a tumour
XX antigen (TAG), where each binding site comprises the variable domains of
XX the light and heavy chains and the heavy domains are connected through a
XX peptide linker. The peptide linker includes at least part of the N-
XX terminus of the CH1 domain of human immunoglobulin G (IgG) and at least
XX part of the Fc domain (or hinge region) is fused to one light
XX chain. A modified antibody contains both of the constant domains of a Fab
XX fragment specific for a tumour, fused to a single-chain Fv antibody
XX (scFv) fragment specific for CD28. Optionally the antibody is also
XX bivalent for TAG and then consists of two antibodies or has a scFv
XX specific for CD28 fused to both heavy chains of a complete anti-TAG
XX antibody. The bispecific antibody dimerises spontaneously, creating a
XX dimer with two binding sites for each antigen. TAG is melanoma-associated
XX proteoglycan, HER-2/neu or CD20. Particularly no stimulation of CTLA-4 on

XX WPI; 2001-246140/26.
DR N-PSDB; AAF61513.
XX
PT Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT variable antibody fragment.
XX
PS Claim 1; Fig 5; 18pp; German.
XX
CC This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and Hela (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transfection. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for Hela,
CC showing the high selectivity for human T cells. This sequence represents
CC the SNV-env leader/human 6C3-scFv fusion construct used in the
CC construction of novel cell targeting vectors described in the invention.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 302 AA;

Query Match 58.2%; Score 1004; DB 4; Length 302;
Best Local Similarity 63.6%; Pred. No. 1.5e-53;
Matches 196; Conservative 47; Mismatches 51; Indels 14; Gaps 4;

QY 1 MDCLTNLRSAGKVDQASKLILLVAWVGFTTAETVSTARAAPMAAEVKLQSQGAEIVR 60
DB 1 MDCLTNLRSAGKVDQASKLILLVAWVGFTTAETVSTARAAPMAAQVLQSQGAEIMK 60

QY 61 PGVSVKISCKGSGYTFDYDQMSWVKQSHAKSLEWIGLSTYYGDPSPNORFKGKATWVD 120
DB 61 PGESLKISCKGFGYDFSTYIAWVRQMPGKLEVMGLIYPGDSDTKYSPSFQCVITISAD 120

QY 121 KSNNTAYLELRLTSDSAYIYCARSQG-----NYGYVYALDYWGQTTVTVSSGGG 172
DB 121 KSISTAYLQWSLSKASDTAMYICARVSGYCSSTSCYDY-YYIYMDVWVGRTLVTVSRGGG 179

QY 173 GSGGGSGGGSGDIELTQSPSSLAVSLGQRATISCRASESDVSVDYSGDSFMHWYQQKPGQPP 232
DB 180 GSGGGSGGGSGDIWMTQSPSTLSASVGRVTVTCRASQINIW----LAWYQQKFGKAP 235

QY 233 KLIYIRASNLIESGVPARFSGSGSESFTLTIDPVEEDDAAVYVCLOSMEDPYTFGGGTKL 292
DB 236 KLIYIRASTLESVPRFSGSGSGTEFTLTISGLQPDFFASYIC-GRYSDWSFGQGTKL 294

QY 293 EIKRAAAS 300
DB 295 EIKRAAAS 302

RESULT 8
AAB20439
ID AAB20439 standard; protein; 729 AA.
XX
AC AAB20439;
XX
DT 21-JUN-2001 (first entry)
XX
DE Antibody 8860-alkaline phosphatase fusion protein.
XX
KW Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;

KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX alkaline phosphatase.
OS Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
PH Key Location/Qualifiers
FT Peptide 1..22 /label= Signal_peptide
FT Protein 23..729 /label= Mature_protein
FT Protein 23..271 /label= scFv
FT Region 23..142 /label= VH
FT Peptide 142..156 /label= Linker
FT Region 157..368 /label= VL
FT Peptide 289..272 /label= Spacer
FT Protein 273..723 /label= Alkaline_phosphatase
FT Peptide 724..729 /label= His_tag
XX
PN W0200119992-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-EP008936.
XX
PR 14-SEP-1999; 99AT-00001576.
XX
PA (BAXT) BAXTER AG.
XX
PI Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX
DR WPI; 2001-290358/30.
DR N-PSDB; AAF30729.
XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
PS Example 16; Fig 29; 138pp; English.
XX
CC The present sequence is that of a fusion protein comprising: a PelB
CC leader; a single chain Fv (scFv) derivative of antibody 8860 comprising
CC the heavy (VH) and light (VL) chain variable regions of antibody 8860
CC joined by an artificial, flexible linker peptide; Escherichia coli
CC alkaline phosphatase; and a C-terminal 6His affinity tail. The DNA was
CC used in the construction of a miniantibody construct (see AAF30730),
CC (FVIII)-like activity of a 198/B1 miniantibody. 198/B1 is an example of
CC anti-human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
CC invention. Anti-FIX/FIXa antibodies and their derivatives have FVIIIa
CC cofactor or FIXa activating activity. Administration leads to an increase
CC in the procoagulant activity of FIXa, even in the presence of FVIIIa
CC inhibitors. This allows for rapid blood coagulation even in the absence
CC of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The
CC antibodies and derivatives are used in a claimed pharmaceutical
CC composition for treating patients with blood coagulation disorders,
CC especially haemophilia A and haemorrhagic diathesis. The scFv-alkaline
CC phosphatase was expressed in E. coli. It exhibited no FVIII-like activity
XX
SQ Sequence 729 AA;

Query Match 57.6%; Score 993.5; DB 4; Length 729;
Best Local Similarity 75.0%; Pred. No. 1.5e-52;

Matches 195; Conservative 23; Mismatches 39; Indels 3; Gaps 2;	
Qy	41 AAQPAEAEVLQSGAEELVRPGVSVKISCKGSGYFTDYDGMVVKQSHAKSLEWIGLIST 100
Db	16 AAQPAEAEVLQSGPELVKPGASVKISCKASGYAFSSWMNVKQRPQGGLWIGRIYP 75
Qy	101 YYGDPYSNORFKGKATMTVDKSNNTAYLELARLTSEDSAIYYCARSDGNYGYVYALDYWG 160
Db	76 GNGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSVDSAVYFCA--DGNV-YYVAMDYWG 132
Qy	161 QGTTVTVSSGGSGGGGGGGSDIELTQSPSSLAVSLGQRATISCRASESVDSYGDSP 220
Db	133 QGTSVTVSSGGSGGGRASGGGSGQIVLTQSPASLAVSLGQRATISCRASKSVSTSGSY 192
Qy	221 MHWYQKPGOPPKLLIYRASNLSEGVPARFSGSGSDFTLTIDPVEEDDAAVYVYCLQSM 280
Db	193 MHWYQKPGOPPKLLIYLASNLSEGVPARFSGSGGDTLTINHPVEEEDAATYYCOHSR 252
Qy	281 EDPYTFGGGTGLEIKRAAAS 300
Db	253 ELPRTFGGGTGLEIKRAAAA 272
RESULT 9	
ID	AAB20443
XX	AAAB20443 standard; protein; 291 AA.
AC	AAAB20443;
XX	21-JUN-2001 (first entry)
DE	Antibody 8860-myc-tag fusion.
XX	Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW	Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag.
XX	Mus musculus.
OS	Synthetic.
OS	Escherichia coli.
OS	Chimeric.
XX	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..22
FT	/label= Signal_peptide
FT	23..291
FT	/label= Mature_protein
FT	23..268
FT	/label= scFv
FT	23..141
FT	/label= VH
FT	142..156
FT	/label= Linker
FT	157..268
FT	/label= VL
FT	269..271
FT	/label= Spacer
FT	272..283
FT	/label= Myc_tag
FT	284..285
FT	/label= Spacer
FT	286..291
FT	/label= His_tag
XX	WO200119992-A2.
PN	22-MAR-2001.
XX	13-SEP-2000; 2000WO-EP008936.
PF	14-SEP-1999; 99AT-00001576.
XX	(BAXT) BAXTER AG.

XX	Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;
PI	WPI; 2001-290358/30.
XX	N-PSDB; AAF30734.
DR	New factor IX/factor IXa antibodies and their derivatives useful for
PT	increasing amidolytic activity of factor IXa, and for treating blood
PT	coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX	Example 18; Fig 35; 138pp; English.
PS	The present sequence is that of a fusion protein comprising: a PeIB
XX	leader; a single chain Fv (scFv) derivative of antibody 8860 comprising
CC	the heavy (VH) and light (VL) chain variable regions of 8860 joined by an
CC	artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a
CC	spacer; and a C-terminal 6His affinity tail. The construct was expressed
CC	in Escherichia coli from vector pMycHis6 and used as negative control in
CC	determinations of the Factor-VIII (FVIII)-like activity of a 198/B1 scFv
CC	also expressed from pMycHis6. 198/B1 is an example of anti-human Factor
CC	IX (FIX)/activated Factor IX (FIXa) antibodies of the invention. Anti-
CC	FIX/FIXa antibodies and their derivatives, including scFv fragments, have
CC	FVIIIa cofactor activity or FIXa activating activity. Administration
CC	leads to an increase in the procoagulant activity of FIXa, even in the
CC	presence of FVIIIa inhibitors. This allows for rapid blood coagulation
CC	even in the absence of FVIII or FVIIIa, and in the case of FVIII
CC	inhibitor patients. The antibodies and derivatives are used in a claimed
CC	pharmaceutical composition for treating patients with blood coagulation
CC	disorders, especially haemophilia A and haemorrhagic diathesis
XX	Sequence 291 AA;
SQ	Query Match 57.5%; Score 992.5; DB 4; Length 291;
	Best Local Similarity 75.3%; Pred. No. 7.2e-53;
	Matches 195; Conservative 22; Mismatches 39; Indels 3; Gaps 2;
Qy	41 AAQPAEAEVLQSGAEELVRPGVSVKISCKGSGYFTDYDGMVVKQSHAKSLEWIGLIST 100
Db	16 AAQPAEAEVLQSGPELVKPGASVKISCKASGYAFSSWMNVKQRPQGGLWIGRIYP 75
Qy	101 YYGDPYSNORFKGKATMTVDKSNNTAYLELARLTSEDSAIYYCARSDGNYGYVYALDYWG 160
Db	76 GNGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSVDSAVYFCA--DGNV-YYVAMDYWG 132
Qy	161 QGTTVTVSSGGSGGGGGGGSDIELTQSPSSLAVSLGQRATISCRASESVDSYGDSP 220
Db	133 QGTSVTVSSGGSGGGRASGGGSGQIVLTQSPASLAVSLGQRATISCRASKSVSTSGSY 192
Qy	221 MHWYQKPGOPPKLLIYRASNLSEGVPARFSGSGSDFTLTIDPVEEDDAAVYVYCLQSM 280
Db	193 MHWYQKPGOPPKLLIYLASNLSEGVPARFSGSGGDTLTINHPVEEEDAATYYCOHSR 252
Qy	281 EDPYTFGGGTGLEIKRAAAA 299
Db	253 ELPRTFGGGTGLEIKRAAA 271
RESULT 10	
ID	AAB20440
XX	AAAB20440 standard; protein; 322 AA.
AC	AAAB20440;
XX	21-JUN-2001 (first entry)
DE	Antibody 8860 bivalent miniantibody.
XX	Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
KW	Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW	bivalent antibody.
XX	Mus musculus.

OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal_peptide
FT /note= "PelB leader"
FT Protein 23..322
FT /label= Mature_protein
FT Protein 23..268
FT /label= scFv
FT Region 23..141
FT /label= VH
FT Peptide 142..156
FT /label= Linker
FT Region 157..268
FT /label= VL
FT Peptide 269..271
FT /label= Spacer
FT Protein 272..281
FT /label= Hinge
FT Protein 282..316
FT /label= Helix
FT Peptide 317..322
FT /label= His_tag
XX
PN WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP008936.
XX
XX 14-SEP-1999; 99AT-00001576.
XX
XX (BAXT) BAXTER AG.
XX
XX Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX
XX WPI; 2001-290358/30.
DR N-PSDB; AAF30730.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 16; Fig 30; 138pp; English.
XX
XX The present sequence is that of a bivalent miniantibody comprising a PelB
CC leader peptide, the single chain Fv (scFv) fragment of antibody 8860, an
CC amphipathic helical structure and a C-terminal 6His tag. The protein was
CC expressed in Escherichia coli from plasmid p8860-Zip#1.2 (see AAF30730).
CC It was used as negative control in determinations of the factor VIII
CC (FVIII)-like activity of a 198/B1 miniantibody (see AAB20438). 193/B1 is
CC an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC antibodies of the invention. Anti-FIX/FIXa antibodies and their
CC derivatives have FVIIIa cofactor activity or FIXa activating activity.
CC Administration leads to an increase in the procoagulant activity of FIXa,
CC even in the presence of FVIIIa inhibitors. This allows for rapid blood
CC coagulation even in the absence of FVIII or FVIIIa, and in the case of
CC FVIII inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis. The present bivalent miniantibody exhibited no FVIII-like
CC activity
XX
SQ Sequence 322 AA;
Query Match 57.5%; Score 992.5; DB 4; Length 322;
Best Local Similarity 75.3%; Pred. No. 8e-53;
Matches 195; Conservative 22; Mismatches 39; Indels 3; Gaps 2;
XX 41 AAQPAAMAEVKLOQSGAEVLPVGVSVKISCKGSGYTFDTYDGMVSWVKQSHAKSLEWIGLIST 100

Db 16 AAQPAAMAEVKLOQSGPELVKPGASVKISKASGYAFSSWMWVKQPGGLEWIGRIYP 75
Qy 101 YYGDPFSYNORFKGKATMTVDKSNNTAYLELRLTSEDSAIYYCARSDGNYGYVALDYWG 160
Db 76 GNGDTNYNGKFKGKATLTADKSSSTAYMQLSLSLTSVDSAVYFCA--DGNV-YYYAMDYWG 132
Qy 161 QGTTVTVSSGGGGSGGGGGSDIELTQSPSSSLAVSLGQRATISCRASESVDSYGDSP 220
Db 133 QGTSVTVSSGGGGSGGRASGGGQIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSY 192
Qy 221 MEHWYQKQPPKLLIYRASNLSEGVPARFSGSGSEDFTLTIDPVEEDAAVYVCLQSM 280
Db 193 MEHWYQKQPPKLLIYLASNLSEGVPARFSGSGSGTDTLTINHPVEEDAAVYVQHSR 252
Qy 281 EDPYTFGGGTGLEIKRAAA 299
Db 253 ELPRTFGGGTGLEIKRAAA 271
RESULT 11
ADS88777
ID ADS88777 standard; protein; 298 AA.
XX
AC ADS88777;
XX
DT 16-DEC-2004 (first entry)
XX
DE Amino acid sequence of the IC2 scFv antibody from clone p330.
XX
KW G glycoprotein; respiratory syncytial virus;
KW respiratory syncytial virus infection; RSV; RSV infection; IC2; scFv.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /note= "PelB leader sequence"
FT Region 144..158
FT /note= "linker"
FT Region 276..281
FT /note= "His tag"
FT Region 285..295
FT /note= "cmcy tag"
XX
PN WO2004083373-A2.
XX
XX 30-SEP-2004.
XX
XX 22-MAR-2004; 2004WO-GB001239.
XX
XX 22-MAR-2003; 2003GB-00006618.
XX
XX (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
XX
XX Toms G, Routledge E, Mekseepalard C;
XX
XX WPI; 2004-691033/67.
DR N-PSDB; ADS88776.
XX
XX New antibody against the G glycoprotein of RSV with a variable region
PT having a first and second domain from a VL and VH region, respectively,
PT useful for treating respiratory syncytial virus (RSV) infections.
XX
XX Example 2; SEQ ID NO 45; 93pp; English.
XX
XX The specification describes an against the G glycoprotein of respiratory
CC syncytial virus, with a variable region comprising a first domain from a
CC variable light chain region and a second domain a variable heavy chain
CC region. The antibodies of the invention are useful for treating and
CC preventing the development of infections caused by the respiratory
CC syncytial virus (RSV). The present sequence represents the IC2 scFv from

CC clone p530. This scFv is an exemplary antibody of the invention. IC2 is a
CC murine monoclonal antibody known to bind to the SV G glycoprotein. IC2
CC was used as a source of sequences to construct antibodies of the
CC invention.

XX SQ Sequence 298 AA;

Query Match 57.4%; Score 991; DB 8; Length 298;

Best Local Similarity 73.5%; Pred. No. 9.1e-53; Indels 2; Gaps 2;

Matches 191; Conservative 27; Mismatches 40; Indels 2; Gaps 2;

QY 41 AAQAPMAEVLKQSGAELVRPGVSVKISCKSGYTFDYGMVWVKQSHAKSLEWIGLIST 100

DB 16 AAQAPMAQVLQSGPEVVRPGVSARISCKSGYTFDYAMHVWVKQSHAKSLEWIGVIST 75

QY 101 YYGDPSPNQRFKQKATMTVDKSSNTAYLELRLTSDSAIYYCARSDG-NYGYYYALDYW 159

DB 76 YYGNPNYNOKFKQKATMTVDKSSNTAYMELARLTIEDSAIYYCARSDMITAGGGYAMDY 135

QY 160 GQGTITVTSSGGSGGGGGGSDIELTQSPSSLAVSLGQRTATISCRASES-VDSYGD 218

DB 136 GQGTITVTSSGGSGGGGGGSAQDVLMTQTPSLPVSIGDQASISCRSSQNVHSDGN 195

QY 219 SFMHYQQRPGQPPKLLIYRASNLGSGVPARFSGSGESDFTLTIDPVEEDAAVYVCLQ 278

DB 196 TYLEWYLKQPGQPPKLLIYKVSNRFSGVPDRFSGSGSGDTFTLKISRVEADLGVYVCFQ 255

QY 279 SMEDPTFGGQTKLEIKRAA 298

DB 256 GSHIPWTFGGGQTKLEISAAA 275

RESULT 12

AAAY50822

ID AAY50822 standard; protein; 554 AA.

XX AC AAY50822;

XX DT 18-FEB-2000 (first entry)

XX DE Fv-antibody construct containing antibody 9E10 epitope protein.

XX KW Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;

XX KW diagnosis; therapy; disease.

XX OS Synthetic.

XX PN DE19819846-A1.

XX PD 11-NOV-1999.

XX PF 05-MAY-1998; 98DE-01019846.

XX PR 05-MAY-1998; 98DE-01019846.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Little M, Kipriyanov S;

XX DR WPI; 2000-024472/03.

XX DR N-PSDB; AA243431.

XX PT Multivalent Fv-antibody constructs with at least four variable domains

XX PT connected by 1, 2 and 3 peptide linkers.

XX PS Example 1; Fig 5; 14pp; German.

XX CC This invention describes a novel multivalent Fv-antibody construct with
CC at least four variable domains that are connected to one another by 1, 2
CC and 3 peptide linkers. The construct has antiviral, antibacterial and
CC cytostatic activity. The multivalent Fv-antibody constructs are useful
CC for the diagnosis and/or therapy of disease, especially viral, bacterial
CC or tumor diseases. The multivalent Fv-antibody constructs have increased

CC stability when in the form of a single chain dimer. This sequence
CC represents a bivalent Fv antibody construct composed of the antibody 9E10
CC epitope in expression plasmid pBISC3x19-LL

XX SQ Sequence 554 AA;

Query Match 57.4%; Score 991; DB 3; Length 554;

Best Local Similarity 69.9%; Pred. No. 1.6e-52;

Matches 197; Conservative 30; Mismatches 45; Indels 10; Gaps 3;

QY 41 AAQAPMAEVLKQSGAELVRPGVSVKISCKSGYTFDYGMVWVKQSHAKSLEWIGLIST 100

DB 16 AAQAPMAQVLQSGAELARPGASVKMSCKASGYTFTRYTMHVWVKQRPQGLEWIGVINP 75

QY 101 YYGDPSPNQRFKQKATMTVDKSSNTAYLELRLTSDSAIYYCARSDGNYGYVYALDYWG 160

DB 76 SRGYTNYNOKFKQKATLTDDKSSNTAYMQLSSLTSDSAVYYCAR---YYDDHYSLDYWG 132

QY 161 QGTTVTVSSGGSGGGGGGSDIELTQSPSSLAVSLGQRTATISCRASESVDYGDGF 220

DB 133 QGTTLTVSSAKTTPKLG-----DILLTQTPLASVSLGQRTATISCKASQSDYDGDY 186

QY 221 MHYQQRPGQPPKLLIYRASNLGSGVPARFSGSGESDFTLTIDPVEEDAAVYVCLQSM 280

DB 187 LNWYQIQPGQPPKLLIYDASNLVSGIPPRFSGSGSGDTFTLNHPVKVDAATYHCQQT 246

QY 281 EDPTFTFGGQTKLEIKRAAASGGSGGS-GGGSGGGSGGGGS 321

DB 247 EDPTFTFGGQTKLEIKRADAAAAGGGSGGGSGGGSGGGGS 288

RESULT 13

AAAY51142

ID AAY51142 standard; protein; 305 AA.

XX AC AAY51142;

XX DT 31-MAR-2000 (first entry)

XX DE Murine derived protein fragment #4.

XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
XX KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
XX KW HIV infection; autoimmune disease; murine.

XX OS Mus sp.

XX PN WO961629-A1.

XX PD 02-DEC-1999.

XX PF 24-MAY-1999; 99WO-JP002711.

XX PR 25-MAY-1998; 98JP-00159957.

XX PR 26-MAY-1998; 98JP-00163023.

XX PA (ASAH) ASAH KASEI KOGYO KK.

XX PA (ASAH) ASAH MEDICAL CO LTD.

XX PI Ono M, Soka T, Morimoto I, Miyamura K;

XX DR WPI; 2000-086720/07.

XX DR N-PSDB; AA244206.

XX PT Devices containing antibodies recognising CD4 or CD34 and their use for
XX PT the separation of CD4 or CD34 positive cells.
XX PS Claim 22; Page 82-84; 11pp; Japanese.

XX CC This invention describes a novel device (I) for separating cluster
CC differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for the

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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 371 Seconds
(without alignments)
85.324 Million cell updates/sec

Title: US-10-089-278-6
Perfect score: 1725
Sequence: 1 MDCLTNLSASGKVDQASKI.....GSGGGGGGGGSGASPQVQFI 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	807	46.8	233	2 JC5322	p53 specific singl
2	798	46.3	249	2 S41374	single chain Fv an
3	783.5	45.4	268	2 A56446	Ig heavy chain V r
4	522	30.3	111	1 KWS37	Ig kappa chain V r
5	516	29.9	131	1 KWSM6	Ig kappa chain pre
6	500	29.0	136	1 HWSB1	Ig heavy chain pre
7	496	28.8	111	2 D45722	anti-glycoprotein
8	495	28.7	107	2 S26344	Ig kappa chain V r
9	493	28.6	115	2 S63596	Ig kappa chain V r
10	485	28.1	107	2 S26343	Ig kappa chain V r
11	485	28.1	112	2 S19976	Ig kappa chain V r
12	482	27.9	111	2 S09965	Ig kappa chain V r
13	480	27.8	111	2 E53285	Ig kappa chain V-J
14	480	27.8	132	1 KWSM32	Ig kappa chain V a
15	478	27.7	112	2 S19972	Ig kappa chain pre
16	477	27.7	137	2 H32513	Ig heavy chain pre
17	476	27.6	111	1 KWSM43	Ig kappa chain V r
18	475	27.5	111	1 KWSM08	Ig kappa chain V r
19	471	27.3	112	2 S19971	Ig kappa chain V r
20	470	27.2	111	1 KWSM83	Ig kappa chain V r
21	470	27.2	111	1 KWSM31	Ig kappa chain V r
22	470	27.2	131	2 PH1226	Ig kappa chain pre
23	468	27.1	111	1 KWSM59	Ig kappa chain V r
24	468	27.1	139	2 A27609	Ig heavy chain pre
25	468	27.1	150	2 F80444	Ig heavy chain V r
26	467	27.1	119	2 F30502	Ig heavy chain V r
27	465	27.0	210	2 A56169	Ig kappa chain V r
28	462.5	26.8	110	1 KWSM10	Ig kappa chain V r
29	461	26.7	111	1 KWSM40	Ig kappa chain V r

30	461	26.7	111	1 KWSM84	Ig kappa chain V r
31	460.5	26.7	119	2 PH0099	Ig heavy chain V r
32	460	26.7	111	1 KWSM80	Ig kappa chain V r
33	458.5	26.6	140	2 S04575	Ig kappa chain pre
34	457	26.5	111	2 S09969	Ig kappa chain V-J
35	455	26.4	111	1 KWSM50	Ig kappa chain V r
36	454	26.3	111	1 KWSM75	Ig kappa chain V r
37	454	26.3	111	2 PL0081	Ig kappa chain V r
38	454	26.3	114	2 S26319	Ig heavy chain V r
39	454	26.3	128	2 C37267	Ig heavy chain V r
40	453	26.3	111	1 KWSM85	Ig kappa chain V r
41	452.5	26.2	144	2 B30502	Ig heavy chain V r
42	448.5	26.0	140	2 T01407	Ig heavy chain (my
43	446	25.9	109	2 PH0093	Ig kappa chain V r
44	446	25.9	111	2 S09963	Ig kappa chain V-J
45	445.5	25.8	117	1 HWSM4E	Ig heavy chain V r

ALIGNMENTS

RESULT 1

JC5322

p53 specific single-chain antibody Pab421 - human

C:Species: Homo sapiens (man)

C>Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C:Accession: JC5322

R:Jannot, C.B.; Hynes, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A:Reference number: JC5322; MUID:97168950; PMID:9016757

A:Accession: JC5322

A:Molecule type: mRNA

A:Residues: 1-233 <JAN>

A:Experimental source: hydrioloma cell

C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 46.8%; Score 807; DB 2; Length 233;

Best Local Similarity 67.5%; Pred. No. 2.1e-41;

Matches 164; Conservative 20; Mismatches 49; Indels 10; Gaps 3;

Qy	52	QQGAELVRPGVSVKISKGGGYFTDYGMSSWKSHAKSLEWIGLSTYGYDPSNQRF	111
Db	1	QESGAELVRGASVKLSCTTSGFNINDYMHVKKRPEQGLEWIGRIDPDNGDADMTRSS	60
Qy	112	KGKATMTVDKSSNTAYLELRLTSEDSAIYCARSDNGNYGYAYALDYMGQGTITVTS	171
Db	61	GVRATMTADTSSNTAYLQLSLTSEDVAVYVC-----NAG-----MDYWGQGTITVTS	111
Qy	172	GGSGGGGGGGSDIELTQSPSSLAVSLGORATISCRASVSDSYGDSFMHWYQKPKQP	231
Db	112	GGSGGRASGGGGSDIELTQSPASLAVSLGORATISCRASKSVSTSGYSYMHWNQKPKQP	171
Qy	232	PKLLIYRASNLSEGVPRFSGSGSESDFTLTIDPVEEDDAVYVCLQSMEDPYTFGGG	291
Db	172	PRLLIYLVNLESGVPRFSGSGSGDFTLTINIHVEEEDAATYYC-QHIRELTSEGG	230
Qy	292	LEI 294	
Db	231	LEI 233	

RESULT 2

S41374

single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: S41374

R:Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv antibody

A:Reference number: S41374

A:Accession: S41374

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:Z29480

Query Match 46.3%; Score 798; DB 2; Length 249;
Best Local Similarity 63.5%; Pred. No. 7.7e-41;
Matches 160; Conservative 29; Mismatches 59; Indels 4; Gaps 2;

Qy 48 EVKLQSQGAELVRPGVSVKISCKSGYTFDYGMVSWKQSHAKSLWIGLISTYIGDPSY 107
Db 1 QVQLQSQGAELVRPGASVKLSCTASGFNFKDDYIHVKQRPKEGLEWIAPIASGNVKY 60

Qy 108 NQRPFGKATWTVKSNNTAYLELRLTSDSAIYYCARSDNGVYVYALDYWGQGTITTV 167
Db 61 VPRFQDKATITADTSSNTAYLLSLTSEDVAVYICARRD---TLYTSLGYNWGQGTITV 117

Qy 168 SSGGG 226
Db 118 SSRGG 177

Qy 227 KPGOPPKLLIYRASNLESVGPAREFSGSGESDFTLTIDPVEEDDAVYVCLQSMEDPYTF 286
Db 178 RCGSPQLLIYRMSNLASGVPDRFSGSGSGTFTLRISRVEAEDGVYVCMQHREYPLTF 237

Qy 287 GGGTKLEIKRAA 298
Db 238 GAGTKLEIKRAA 249

RESULT 3
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Yang, P.W.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U0617
C;Keywords: heterotetramer; immunoglobulin

Query Match 45.4%; Score 783.5; DB 2; Length 268;
Best Local Similarity 60.2%; Pred. No. 6e-40;
Matches 154; Conservative 34; Mismatches 55; Indels 13; Gaps 3;

Qy 46 MAEVLQSQGAELVRPGVSVKISCKSGYTFDYGMVSWKQSHAKSLWIGLISTYIGDGP 105
Db 1 MAQVKLQSQGAELVKPGASVKLSCTTSGFNKIDTYMHVWVQRPQGLEWIGRIAPANGIT 60

Qy 106 SYNRPFGKATWTVKSNNTAYLELRLTSDSAIYYCARSDNGVYVYAL--DYWGQGT 163
Db 61 KYDPKFGQKATTAADTSSNTAYLQLSLTSEDVAVYICA-----SYLTTRYENYWGQGT 114

Qy 164 TTVTVSSGG 223
Db 115 TTVTVSSGG 169

Qy 224 YQKPGOPPKLLIYRASNLESVGPAREFSGSGESDFTLTIDPVEEDDAVYVCLQSMEDP 283
Db 170 YQKSDASPKLWVYVYTHLPVGPVAREFSGSGSGNSYSLTSSMEGEDAATYVYVCOQFTSSP 229

Qy 284 YTFGGGTGLEIKRAA 299
Db 230 FTFGGGTGLEIKRSAA 245

RESULT 4

KVMS37
Ig kappa chain V regions (PC3741, T111) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A93204; A93822; A01934
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Contents: PC3741
A;Accession: A93204
A;Molecule type: protein
A;Residues: 1-111 <WEI>
A;Cross-references: UNIPROT:P01660
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: T111
A;Accession: A93822
A;Molecule type: protein
A;Residues: 1-111 <MCK>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 30.3%; Score 522; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 8.9e-25;
Matches 99; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 185 DIELTQSPSSLAVSLGQRATISCRASESVDSYGSFMHWYQKPGQPKLLIYRASNLES 244
Db 1 DIVLTQSPASLAVSLGQRATISCRASESVDSYGSFMHWYQKPGQPKLLIYRASNLES 60

Qy 245 GVPAFESGSGESDFTLTIDPVEEDDAVYVCLQSMEDPYTFGGGTGLEIK 295
Db 61 GIPARFSGSGSRDTLTITINPVEADVDVATYYCQSNEDPYTFGGGTGLEIK 111

RESULT 5
KVMSM6
Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: B90412; B90374; B93822; C93204; D93204; D93204; PH1078; A01935
R;Burstein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A;Title: Primary structures of N-terminal extra peptide segments linked to the variable
expression of immunoglobulin genes.
A;Reference number: A90412; MUID:78235887; PMID:98179
A;Contents: M63
A;Accession: B90412
A;Molecule type: protein
A;Residues: 1-35 <BUR>
A;Cross-references: UNIPROT:P01661
R;McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
A;Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains w
A;Reference number: A90374; MUID:73140225; PMID:4691517
A;Contents: M63
A;Accession: B90374
A;Molecule type: protein
A;Residues: 1-46, 'Q', 48-53, 'B', 55-57, 'Z', 59-86, 'F', 88-131 <MCK>
A;Note: This sequence has since been revised in reference A93822
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A;Reference number: A93822; MUID:79012520; PMID:99744
A;Contents: M63; AB22
A;Accession: B93822

A:Molecule type: protein
A:Residues: 1-53;69-107 <MC2>
A:Accession: C93822
A:Molecule type: protein
A:Residues: 21-119,'Y',121-131 <MC3>
A:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Contents: PC9245; PC4050
A:Accession: C93204
A:Molecule type: protein
A:Residues: 21-119,'Y',121-131 <WE1>
A:Accession: D93204
A:Molecule type: protein
A:Residues: 21-119,'L',121-123,'A',125-129,'L',131 <WE2>
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1078
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 21-122 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
A:Comment: The M63 precursor sequence is shown.
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status experimental <SIG>
F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>
F:43-112/Disulfide bonds: #status predicted

Query Match 29.9%; Score 516; DB 1; Length 131;
Best Local Similarity 86.1%; Pred. No. 2.4e-24;
Matches 99; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 181 GGSDIELTQSPSLAVSLGQRATISCRASESDVSDGSDFMHWYQKPGQPPKLLIYRAS 240
Db 17 GSTGNIVLTQSPASLAVSLGQRATISCRASESDVSDGSDFMHWYQKPGQPPKLLIYLAS 76

Qy 241 NLESGVPARFSGSGSEDFLTIDPVEEDAAVYICQSMEDPPTFGGTTKLEIK 295
Db 77 NLESGVPARFSGSGSRDFTLTIDPVEADDAATYICQNNEDPPTFGGTTKLEIK 131

RESULT 6
HVM581
Ig heavy chain precursor V region (BC11) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-1992 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A02042
R:Knapp, M.R.; Liu, C.P.; Newell, N.; Ward, R.B.; Tucker, P.W.; Strober, S.; Blattner, P
Proc. Natl. Acad. Sci. U.S.A. 79, 2996-3000, 1982
A:Title: Simultaneous expression of immunoglobulin mu and delta heavy chains by a clone
A:Reference number: A02042; MUID:62222262; PMID:6806821
A:Accession: A02042
A:Molecule type: mRNA
A:Residues: 1-136 <KNA>
A:Cross-references: UNIPROT:P01759; GB:J00494; NID:9195010; PIDN:AAA38130.1; PID:g195011
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-136/Product: Ig heavy chain V region (BC11) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 29.0%; Score 500; DB 1; Length 136;
Best Local Similarity 73.9%; Pred. No. 2.2e-23;

Matches 99; Conservative 12; Mismatches 15; Indels 8; Gaps 2;
Qy 36 VSTARAAQPAEAEVYKLOQSGAELVRPGVSVKISKCKSGYTFDYGMVVKQSHAKSLEWI 95
Db 11 VATATGVH---SQVQLQQSGPEVVRPGVSVKISKCKSGYTFDYAMHVKQSHAKSLEWI 67

Qy 96 GLISTYYGDSNORFKGKATMTVDKSNATAYLRLTSDSAIYYCARSDGNYGYA 155
Db 68 GVISTYNGNTSYNQKFKGKATMTVDKSSSTVHMLARLTSDSANLYCARYGNY----- 122

Qy 156 LDYWGQGTITVTSS 169
Db 123 FDYWGQGTITVTSS 136

RESULT 7
D45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse (f
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: D45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: D45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-111 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBI:120592)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 28.8%; Score 496; DB 2; Length 111;
Best Local Similarity 86.5%; Pred. No. 3.1e-23;
Matches 96; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 185 DIELTQSPSLAVSLGQRATISCRASESDVSDGSDFMHWYQKPGQPPKLLIYRASLES 244
Db 1 NIVLTQSPASLAVSLGQRATISCRASESDVSDGSDFMHWYQKPGQPPKLLIYLASNLES 60

Qy 245 GVPARFSGSGSEDFLTIDPVEEDAAVYICQSMEDPPTFGGTTKLEIK 295
Db 61 GVPTRFSGSGSRDFTLTIDPVEADDAATYICQNNEDPRTFGGTTKLEIK 111

RESULT 8
S26344
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26344
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26344
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59209; NID:952336; PIDN:CAA41919.1; PID:g1334074
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 28.7%; Score 495; DB 2; Length 107;
Best Local Similarity 87.6%; Pred. No. 3.5e-23;
Matches 92; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 188 LTQSPSLAVSLGQRATISCRASESDVSDGSDFMHWYQKPGQPPKLLIYRASNLSSGVP 247
Db 3 MTQTPASLAVSLGQRATISCRASESDVSDGSDFMHWYQKPGQPPKLLIYRASNLSSGIP 62

```
QY 248 ARFSGSGSDFTLTIDPVEEDAAVYCYCLOSMEDPVTGGGSKL 292
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 ARFSGSGSRTDFTLTINPVEADDAVATYCYCQSNEDPVTGGGSKL 107

RESULT 9
S63596
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S63596
R:Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Fita, I.
J. Mol. Biol. 256, 364-376, 1996
A>Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutralized antigen-binding site
A:Reference number: S63596; MUID:96174482; PMID:8594203
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-115 <VER>
A:Cross-references: GB:S61196; NID:gl336821; PIDN:AAB36171.1; PID:gl336822
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 28.6%; Score 493; DB 2; Length 115;
Best Local Similarity 83.5%; Pred. No. 4.9e-23;
Matches 96; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 185 DIETQSPSSLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 244
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPASLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 60

QY 245 GVPARFSGSGSDFTLTIDPVEEDAAVYCYCLOSMEDPVTGGGSKLEIKRAA 299
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GIPDRFSGSGSRTDFTLTIDPVEADDAVATYCYCQSNEDPVTGGGSKLEIKRADA 115

RESULT 10
S26343
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26343
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A>Title: Antibodies that are specific for a single amino acid interchange in a protein encoded by the B220 gene
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26343
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59207; NID:g52334; PIDN:CAA1917.1; PID:gl334073
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 28.1%; Score 485; DB 2; Length 107;
Best Local Similarity 85.7%; Pred. No. 1.4e-22;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 188 LTQSPSSLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 MTQTPASLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 62

QY 248 ARFSGSGSDFTLTIDPVEEDAAVYCYCLOSMEDPVTGGGSKL 292
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 ARFSGSGSRTDFTLTINPVEADDAVATYCYCQSNEDPVTGGGSKL 107

RESULT 11
S19976
Ig kappa chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
```

```
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19976
R:Weissenborn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19976
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
```

```
Query Match 28.1%; Score 485; DB 2; Length 112;
Best Local Similarity 81.2%; Pred. No. 1.4e-22;
Matches 91; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 185 DIETQSPSSLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 244
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPASLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 60

QY 245 GVPARFSGSGSDFTLTIDPVEEDAAVYCYCLOSMEDPVTGGGSKLEIKR 296
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GIPARFSGSGSRTDFTLTINPVEEDAAVATYCYCQSIQDPYTFGGGSKLEIKR 112
```

```
RESULT 12
S09965
Ig kappa chain V-J region (106-10E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: S09965
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A>Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A:Reference number: S09955; MUID:90269328; PMID:2347362
A:Accession: S09965
A:Molecule type: mRNA
A:Residues: 1-111 <REI>
A:Cross-references: EMBL:X51853; NID:g55394; PIDN:CAA36146.1; PID:g930230
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
```

```
Query Match 27.9%; Score 482; DB 2; Length 111;
Best Local Similarity 82.9%; Pred. No. 2.1e-22;
Matches 92; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 185 DIETQSPSSLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 244
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPASLAIVSLGQRATISCRASESDVSDGSMHMYQKPGQPPKLLIYRASNL 60

QY 245 GVPARFSGSGSDFTLTIDPVEEDAAVYCYCLOSMEDPVTGGGSKLEIK 295
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GIPARFSGSGSRTDFTLTINPVEADDAVATYCYCQSNEDPVTGGGSKLEIK 111
```

```
RESULT 13
E53285
Ig kappa chain V and J regions, monoclonal antibody OHP 4B2.2.1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: E53285
R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A>Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structures and their pH-reactivity profiles.
A:Reference number: A53285; MUID:92017897; PMID:1922102
A:Accession: E53285
A>Status: preliminary
A:Molecule type: DNA; protein
```

```

QY 241 NLSEGVPAFPFGSGSSDFTLTIDPVEEDAAVYVYCLQSMEDPYTFGGGKLEIKR 296
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77 NLZSGIPARFSGSGSRTBFTLTIBPVZABDVATYFCZZSBZBPTFGSGTKLEIKR 132

RESULT 15
S19972
IG kappa chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19972
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Accession: S19972
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <WE1>
A;Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 27.7%; Score 478; DB 2; Length 112;
Best Local Similarity 82.1%; Pred. No. 3.7e-22;
Matches 92; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 185 DIELTQSPSSLAVSLGQRATISCRASESVDSYGDSPMHVYQOKPGOPPKLLIYRASNLES 244
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPASLAVSLGQRATIFCRASQSDVDYNAISYMHVYQOKPGOPPKLLIYRASNLES 60

QY 245 GVPARFSGSGSSDFTLTIDPVEEDAAVYVYCLQSMEDPYTFGGGKLEIKR 296
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GIPARFSGSGSGTDFTLIDHPVEEDAAVYVYVYQSSSDPYTFGGGKLEIKR 112

Search completed: August 23, 2005, 11:23:48
Job time : 372 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 1917 Seconds
(without alignments)
87.884 Million cell updates/sec

Title: US-10-089-278-6
Perfect score: 1725
Sequence: 1 MDCLTLNLSRABGKVDQASKI.....GSGGGGGGGGSGASPVQFI 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	800.5	46.4	244	2 Q65ZC8	Q65zc8 homo sapien
2	773.5	44.8	243	2 Q7TQW2	Q7Tqm2 mus musculus
3	768.5	44.6	487	2 Q85ZL2	Q85z12 mus sp. fv/
4	763	44.2	298	2 Q9QYF0	Q9qyf0 synthetic c
5	762.5	44.2	241	2 Q921A6	Q921a6 mus musculus
6	760.5	44.1	255	2 Q6KB05	Q6kb05 mus musculus
7	744.5	43.2	240	2 Q65ZC9	Q65zc9 homo sapien
8	744	43.1	248	2 Q85ZQ7	Q85zq7 mus sp. b3(
9	737	42.7	218	2 Q925S1	Q925s1 mus musculus
10	607	35.2	170	2 Q925S2	Q925s2 mus musculus
11	522	30.3	111	1 KV3H MOUSE	P01660 mus musculus
12	517	30.0	111	1 KV3J MOUSE	P01662 mus musculus
13	516	29.9	131	1 KV3I MOUSE	P01661 mus musculus
14	501	29.0	111	1 KV3K MOUSE	P01663 mus musculus
15	500	29.0	136	1 HV15 MOUSE	P01759 mus musculus
16	480	27.8	132	1 KV3F MOUSE	P01658 mus musculus
17	476	27.5	111	1 KV3M MOUSE	P01665 mus musculus
18	475	27.5	111	1 KV3O MOUSE	P01667 mus musculus
19	472	27.4	111	2 Q811U6	Q811u6 mus musculus
20	470	27.2	111	1 KV3L MOUSE	P01664 mus musculus
21	470	27.2	111	1 KV3N MOUSE	P01666 mus musculus
22	470	27.2	111	2 Q920S9	Q920s9 mus musculus
23	469	27.2	112	1 KV3G MOUSE	P01659 mus musculus
24	468	27.1	111	1 KV3Q MOUSE	P01669 mus musculus
25	464.5	26.9	117	2 Q9QXE9	Q9qxe9 mus musculus
26	462.5	26.8	110	1 KV3P MOUSE	P01668 mus musculus
27	462.5	26.8	470	2 Q7TMK1	Q7tmk1 mus musculus
28	461	26.7	111	1 KV3R MOUSE	P01670 mus musculus
29	461	26.7	111	1 KV3T MOUSE	P01672 mus musculus
30	460	26.7	111	1 KV3A MOUSE	P01654 mus musculus
31	459	26.6	488	2 Q91WF1	Q91wr1 mus musculus

ALIGNMENTS

RESULT 1

Q65ZC8	PRELIMINARY;	PRT;	244 AA.
AC	Q65ZC8;		
DT	25-OCT-2004 (TrEMBLrel. 28, Created)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Single-chain Fv (Fragment).		
GN	Name=scFv;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97362799; PubMed=9219263;		
RA	Kontermann R.E., Wing M.G., Winter G.;		
RT	"Complement recruitment using bispecific diabodies.";		
RL	Nat. Biotechnol. 15:629-631(1997).		
DR	EMBL; Y13057; CAA73500.1; -.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 2.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00406; IGv; 2.		
DR	PROSITE; PS00835; IG_LIKE; 2.		
FT	NON TER 1		
FT	NON TER 244		
SQ	SEQUENCE 244 AA; 26127 MW; 4B1F17868339F2BF CRC64;		
Query Match 46.4%; Score 800.5; DB 2; Length 244;			
Best Local Similarity 60.6%; Pred. No. 3.8e-48;			
Matches 151; Conservative 39; Mismatches 54; Indels 5; Gaps 2;			
Qy	48	EVKLQSGAEIVRCVSVKISCKSGYTFDYGNSWVKQSHAKSLWIGLISITYGDP	SY 107
Db	1	QVQLVQSGAEVRCVSGSVKSKASGYTFSDHYMHYWRQAPGQGLEWMGIDPNNGD	TRF 60
Qy	108	NQRFKQATMTVDKSNNTAYLELARTLSEDAIYICARSDGNYYVYALDVGQGT	TVV 167
Db	61	AQRFQGVMTWRTDTSISAAYMEVSRLLSDDTAVYICAR-EGTGSATYGMVWGQ	TLTV 119
Qy	168	SSGGGGGGGGGGGGSDIELTQSPSLAVSLGQRATISCRASVSDSYGDSFMHWYQ	QOK 227
Db	120	SSGGGGGGGGGGGGSDIQMTQSPSTLSASIGDRVITCRASGEIYHW----LAWYQ	OK 175
Qy	228	PGPPKLLIIRANLSGVPARFSGSGESDFTLTIDPVEDDAVYICLQSMEDPTFG	287
Db	176	PGKAPFLIYKASLSASGAPRFSGSGGTDTLTITSSLPQDFPATYICQYQSNYP	PLTF 235
Qy	288	GGTKLEIKR 296	
Db	236	GGTKLEIKR 244	

Qy	168	SSGGGGGGGGGGGGSDIELTQSPSSLASVLSLQORATISCRASESVDSYGDSFMHWYQOK	227		
Db	117	SSGGGGGGGGGGGGSDIELTQSPSSLASLGGKVITTKASQDINKY-----IAWYQHK	172		
Qy	228	PGQPPK-----LLIYRASNLSSGVPARESGGSBESDFTLTIDPVEDAAVYCYCLOSMEDP	283		
Db	173	PGGKPSAHTLHIY-----IQGIPSRFSGSGSGRDYSFSLNLEPDIATYCYLH-YDNL	227		
Qy	284	YTFGGGTGLEIKRA	297		
Db	228	HTFGGGTGLEIKRA	241		
RESULT 6					
Q6KB05	PRELIMINARY; PRT; 255 AA.				
ID	Q6KB05				
AC	Q6KB05				
DT	05-JUL-2004 (T-EMBLrel. 27, Created)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)				
DE	ScFv B8E5 protein (Fragment).				
GN	Name=scFv B8E5;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Balb/c;				
RA	Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,				
RA	Briand J.P., Hoebeke J.;				
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; AJ746180; CAG34081.1; .-				
DR	HSSP; P01837; 1KCR.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	SMART; SM00409; IG_2.				
DR	SMART; SM00406; IG; 2.				
DR	PROSITE; PS50835; IG LIKE; 2.				
FT	NON TER 1				
SQ	SEQUENCE 255 AA; 27445 MW; B68BD38J95DF713B CRC64;				
Query Match 44.1%; Score 760.5; DB 2; Length 255;					
Best Local Similarity 58.4%; Pred. No. 2.5e-45;					
Matches 149; Conservative 38; Mismatches 55; Indels 13; Gaps 4;					
Qy	48	EVKLQSGAELVPPGVSVKISKCGGYTFDYDGMVWKQSHAKSLEWIGLIS-----YY	102		
Db	1	QVQLQSGDGLVPGGSLKVSCTAASGFTFSSYGMVWRQTFDRKLEWVAITSGGSYYT	60		
Qy	103	GDPSYNQRFGKATMTVDKSSNTAYLELARLTSEDSAIYYCARSDGNVYVYALDYWGQ	162		
Db	61	PD-----SVKGRFTISRDNAKNTLYIQMSLKSDATMYICARHI-NRYDGAFDYWGQ	114		
Qy	163	TTVTSSGGGGGGGGGGSDIELTQSPSSLASVLSLQORATISCRASESV--DSYGDSE	220		
Db	115	TTLTVTSSGGGGGGGGGGSDIVMAQSPSSLVSAGAKVMSCKSSQSLNLSRNQNY	174		
Qy	221	MHWYQKQGPQPKLLIYRASNLSSGVPARESGGSBESDFTLTIDPVEDAAVYCYCLOSM	280		
Db	175	LAWYQKQGPQPKLLIYGASTRESGVPDRFTGSGSGDTFLTITISSVQAEADLAVYQCNDH	234		
Qy	281	EDPYTEGGGTGLEIK	295		
Db	235	SYPLTFGAGTGLEIK	249		
RESULT 7					
Q65ZC9	PRELIMINARY; PRT; 240 AA.				
ID	Q65ZC9				
AC	Q65ZC9;				
DT	25-OCT-2004 (T-EMBLrel. 28, Created)				

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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RA MEDLINE=97362799; PubMed=9219263;
RX Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 43.2%; Score 744.5; DB 2; Length 240;
Best Local Similarity 57.4%; Pred. No. 3e-44;
Matches 143; Conservative 40; Mismatches 57; Indels 9; Gaps 2;

Qy 48 EVKLQSGAEIVRPGVSKISCKSGYTFDTYGMVWKSHAKSLEWIGLISITYGDPYS 107
Db 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFSYGHVWRQAPGKLEWVAIVSDGSKYY 60

108 NQRFKGTMTVDKSSNTAYLELARTSEDSAIYYCARSDGNYGYVYALDYWGQGTITVTV 167
61 ADSVKGRTISRDNKNTLYLQMSRLKSEDATVYYCARDWGD----SLDPWGKGLTVTV 115

168 SSGGGSGGGSGGGGGGSDIELTQSPSLAVSLGQRATISCRASBSVDYSGDSFMHWYQQ 227
116 SSGGGSGGGSGGGGGGSDIQWTSPLSLPVSIGRVTITCRASEGIYRW----LAWYQQ 171

228 PGQPPKLLIYRASNLSEGVPARFSGSGSESDFTLTIDPVEEDDAVYVYCLQSMEDPYTF 287
172 PGKAPKLLIYKASLASRAPRFSGSGSGTDTLTLSLQPDPTATYYCOQSYNPLTFG 231

288 GGTGLEIKR 296
232 GGTGLEIKR 240

RESULT 8
Q65ZQ7
ID Q65ZQ7 PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 248 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 43.1%; Score 744; DB 2; Length 248;
Best Local Similarity 59.0%; Pred. No. 3.4e-44;
Matches 147; Conservative 37; Mismatches 61; Indels 4; Gaps 3;

Qy 48 EVKLQSGAEIVRPGVSKISCKSGYTFDTYGMVWKSHAKSLEWIGLISITYGDPYS 107
Db 2 DVKLVESGGGLVQPGSLKLSCATSGTFTSDYYMYWRQTPKRLLEWVAIVSDDSSAY 61

108 NORFKGTMTVDKSSNTAYLELARTSEDSAIYYCARSDGNYGYVYALDYWGQGTITVTV 167
62 SDTVKGRFTISRDNARNTLYLQMSRLKSEDATVYYSCARGLA-WGAWFA--YWGQGLTVTV 118

168 SSGGGSGGGSGGGGGGSDIELTQSPSLAVSLGQRATISCRASE-SVDSYGDSPMHYQQ 226
119 SSGGGSGGGSGGGGGGSDVLTQSPSLPVSIGRVTITCRSSQIIVHSGNTYLEMYLQ 178

227 KGPQPPKLLIYRASNLSEGVPARFSGSGSESDFTLTIDPVEEDDAVYVYCLQSMEDPYTF 286
179 KPQSPKLLIYKVSNSRFGVDPDRFSGSGTDTLTLSRVEADLGVYVYCFQSHVPTTF 238

287 GGTGLEIK 295
239 GGTGLEIK 247

RESULT 9
Q925S1
ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR HSSP; P01665; IQNZ.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;

Query Match 42.7%; Score 737; DB 2; Length 218;
Best Local Similarity 64.4%; Pred. No. 9e-44;
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Matches 143; Conservative 31; Mismatches 44; Indels 4; Gaps 1;
QY 46 MAEYKLOQSGAELVRPGVSKISCKSGYTTFTDYGMSWVKSHAKSLEWIGLISTYGDGP 105
Db 1 MAQVKLOQSGPELVKPGTVAISCKASGYTTTACGMQVQKMPGKGLKMGINTHSGVP 60
QY 106 SYNORFKGATMTVDKSNATYLAELARLTSDSAIYYCARSDGNVGYVYALDYGQGTTV 165
Db 61 KYAEFGKRFAPFASLETASNTAYLQISLNKEDTATYFCMRWDYDGGP----AYWGQGTTV 116
QY 166 TVSSGGGGGGGGGGGGSDIELTQSPSSLAVSLGQRATISCRASESDVSDYGSDFMHWYQ 225
Db 117 TVSSGGGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASESDVSDYGSDFMHWYQ 176
QY 226 QKQOPPKLLIYRASNLGSGVPAFSGSGSESDFTLIDPVE 267
Db 177 QKQOPPKLLIYASKQSGVGPAGLLASGSGTDFSLNIYPME 218

RESULT 10
Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
  Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
  the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
  of the irradiated mice by treatment with the intestinal RNA of mice of
  the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -.
DR HSP; P01751; IAGW.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 35.2%; Score 607; DB 2; Length 170;
Best Local Similarity 73.4%; Pred. No. 8e-35;
Matches 116; Conservative 17; Mismatches 21; Indels 4; Gaps 2;
QY 46 MAEYKLOQSGAELVRPGVSKISCKSGYTTFTDYGMSWVKSHAKSLEWIGLISTYGDGP 105
Db 1 MAQVKLOQSGPELVKPGVSKISCKSGYTTFTDYSMEHLKXNHAQSLEWIGLISTYDGT 60
QY 106 SYNORFKGATMTVDKSNATYLAELARLTSDSAIYYCARSDGNVGYVYALDYGQGTTV 165
Db 61 NYNOKFGKATMTVDKSNATYLAELARLTSDSAIYYCARSDGNVGYVYALDYGQGTTV 119
QY 166 TVSSGGGGGGGGGGGGSDIELTQSPSSLAVSLGORA 203
Db 120 TVSSGGGGGGGGGGGGSGSE-----SSPGGKLEIKRAA 154

RESULT 11
KV3H_MOUSE
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ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gamaian L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
  related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
DR PIR; A93204; KWS37.
DR HSP; P01665; IONZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
RW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 30.3%; Score 522; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 4.2e-29;
Matches 99; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 185 DIELTQSPSSLAVSLGQRATISCRASESDVSDYGSDFMHWYQKQGPCKLIYRASNL 244
Db 1 DIVLTQSPASLAVSLGQRATISCRASESDVSDYGSDFMHWYQKQGPCKLIYRASNL 60
QY 245 GVPARFSGSGSESDFTLTIDPVEDDAAVYVYCLQSMEDPYTFGGGKLEIK 295
Db 61 GIPARFSGSGSRDFTLTINPVEADVDVATYCCQSNEDPYTFGGGKLEIK 111

RESULT 12
KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
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RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RN Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -I- MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical.
DR HSP; P01665; IONZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 30.0%; Score 517; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 9.4e-29;
Matches 99; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 185 DIETQSPSLAVSLGQRATISCRASESVDSYGSFMHWYQQKPGQPKLLIYASNLES 244
Db 1 NIVLTQSPASLAVSLGQRATISCRASESVDSYGSFMHWYQQKPGQPKLLIYASNLES 60

Qy 245 GVPARFSGSGSEDTLTIDPVEDDAAVYVYCLQSMEDPYTSGGKLEIK 295
Db 61 GVPARFSGSGSRDTLTIDPVEADDAATYVYQQNNEDPYTFGGGKLEIK 111

RESULT 13
KV3I_MOUSE
ID _KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to the
RT variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled expression
RT of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
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RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR HSP; P01665; IONZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 Ig kappa chain V-III region MOPC 63.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 58 Complementarity-determining-1.
FT DOMAIN 59 73 Framework-2.
FT DOMAIN 74 80 Complementarity-determining-2.
FT DOMAIN 81 112 Framework-3.
FT DOMAIN 113 121 Complementarity-determining-3.
FT DOMAIN 122 131 Framework-4.
FT DISULFID 43 112 By similarity.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 29.9%; Score 516; DB 1; Length 131;
Best Local Similarity 86.1%; Pred. No. 1.3e-28;
Matches 99; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 181 GGGSDIELTQSPSLAVSLGQRATISCRASESVDSYGSFMHWYQQKPGQPKLLIYRAS 240
Db 17 GSGTNIVLTQSPASLAVSLGQRATISCRASESVDSYGSFMHWYQQKPGQPKLLIYRAS 76

Qy 241 NLESGVPAFSGSGSESDFTLTIDPVEDDAAVYVYCLQSMEDPYTSGGKLEIK 295
Db 77 NLESGVPAFSGSGSRDTLTIDPVEADDAATYVYQQNNEDPYTFGGGKLEIK 131

RESULT 14
KV3K_MOUSE
ID _KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR HSP; P01665; IONZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
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SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 29.0%; Score 501; DB 1; Length 111;
Best Local Similarity 86.5%; Pred. No. 1.2e-27;
Matches 96; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 185 DIETQSPSSLAIVSLGQRATISCRASESVDSYGDSFMHWYQOKPGQPPKLLIYRASNLES 244
Db 1 NIVLTQSPASLAIVSLGQRATISCRASESVDSYGDSFMHWYQOKPGQPPKLLIYLASNLES 60
Qy 245 GVPARFSGSGSEDTLTIDPVEEDDAAYVYCLOSMEDPYTFGGTKLEIK 295
Db 61 GVPARFSGSGSRDPTLTIDPVEADDAATYCCQNNEDPLTFGAGTKLELK 111

RESULT 15

HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared by
two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00494; AAA38130.1; -;
DR PIR; A02042; HVMSB1.
DR HSSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 Ig heavy chain V region BCL1.
FT DOMAIN 20 135 Ig-like.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35B CRC64;

Query Match 29.0%; Score 500; DB 1; Length 136;
Best Local Similarity 73.9%; Pred. No. 1.8e-27;
Matches 99; Conservative 12; Mismatches 15; Indels 8; Gaps 2;

Qy 36 VSTARAAQAMAEVKLQSGAEIVRPGVSVKISCKGSGYFTFDYGMVWVKQSHAKSLEWI 95
Db 11 VATATGVH---SQVLQSGGEVVRPGVSVKISCKGSGYFTFDYAMHWVWVKQSHAKSLEWI 67
Qy 96 GLISTYYGDPSPYQRFKGAATMTYDKSNTAYLEARLTSEDSAIYYCARSDGNYGYAA 155
Db 68 GVIISTYNGNTSYNQKFGKATMTVDKSSSTVHMEARLTSEDSANLYCARYGNY----- 122

Qy 156 LDYWGQGTITVTSS 169
Db 123 FDYWGQGTITVTSS 136

Search completed: August 23, 2005, 12:01:28
Job time : 1919 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2005, 11:17:23 ; Search time 318 Seconds

(without alignments)
77.231 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNRAGKVDQASKI.....GSGGGGGGGSGGASPVQFI 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	56.7	260	2	US-08-447-402-1
2	946.5	54.9	271	2	US-08-894-922A-10
3	923	53.5	267	4	US-09-419-788-30
4	918.5	53.2	297	4	US-09-486-814A-2
5	916.5	53.1	252	2	US-08-894-922A-14
6	914	53.0	269	3	US-09-070-408-132
7	908	52.6	673	3	US-09-423-439-32
8	894.5	51.9	273	2	US-08-403-853-18
9	878	50.9	288	3	US-09-423-439-38
10	873	50.6	353	4	US-09-203-958A-4
11	853.5	49.5	258	4	US-09-526-738A-4
12	844.5	49.0	256	4	US-09-526-738A-2
13	842	48.8	244	2	US-08-553-497A-20
14	837.5	48.6	239	2	US-08-553-497A-18
15	836.5	48.5	666	3	US-09-423-439-51
16	836	48.5	241	4	US-09-581-345-5
17	833.5	48.3	553	2	US-08-661-052-16
18	833.5	48.3	553	3	US-09-188-082-16
19	833.5	48.3	553	3	US-09-364-088-16
20	833.5	48.3	553	3	US-09-102-716-16
21	831	48.2	267	3	US-09-485-737B-2
22	831	48.2	267	4	US-10-071-485-2
23	826	47.9	240	1	US-08-488-113B-148
24	826	47.9	240	1	US-08-477-484B-148
25	826	47.9	240	2	US-08-646-360-148
26	826	47.9	240	3	US-08-839-765-148
27	826	47.9	240	3	US-09-136-389-148

28 826 47.9 240 3 US-09-610-838-148 Sequence 148, App
29 826 47.9 240 4 US-09-711-485-148 Sequence 148, App
30 825 47.8 246 2 US-08-553-497A-24 Sequence 24, Appl
31 823.5 47.7 239 3 US-08-279-772A-8 Sequence 8, Appl
32 823.5 47.7 239 3 US-08-902-486-11 Sequence 11, Appl
33 823 47.7 637 1 US-08-235-838-16 Sequence 16, Appl
34 823 47.7 637 2 US-08-465-473B-16 Sequence 16, Appl
35 822 47.7 244 2 US-08-553-497A-22 Sequence 22, Appl
36 821.5 47.6 252 1 US-08-133-804-4 Sequence 4, Appl
37 821.5 47.6 252 1 US-08-461-838-4 Sequence 4, Appl
38 821.5 47.6 252 2 US-08-461-386-4 Sequence 2, Appl
39 821.5 47.6 270 2 US-08-652-507-2 Sequence 1, Appl
40 820 47.5 244 4 US-09-244-369B-1 Sequence 1, Appl
41 820 47.5 244 4 US-09-940-391-1 Sequence 53, Appl
42 819 47.5 365 3 US-08-875-811-53 Sequence 36, Appl
43 818.5 47.4 240 4 US-10-092-246-37 Sequence 37, Appl
44 818.5 47.4 240 4 US-10-096-246A-37 Sequence 12, Appl
45 816.5 47.3 348 4 US-09-646-028-12

ALIGNMENTS

RESULT 1
US-08-447-402-1
; Sequence 1, Application US/08447402
; Patent No. 5866344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Georgiou, George
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION
; TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED
; LIBRARIES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,402
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,543
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/794,731
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSB:584\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-402-1

[illegible]

FRAGME

	Query Match	54.9%;	Score 946.5;	DB 2;	Length 271;
	Best Local Similarity	70.6%;	Pred. No. 4.6e-60;		
	Matches 192;	Conservative 20;	Mismatches 39;	Indels 21;	Gaps 4
Qy	41	AAQPAMAEVKLQQSGAELVRPGVSVKISCKGSGVTFTDYGMSWKVQSHAKSLIEWGLJST	100		
Db	16	AAQPAMAQVLQQSGAELVRPGVSVKLSCKASDYTFTSYWHWVKRPGQLGEIWEINP	75	:	:
Qy	101	YYGPESYNORFKGATMVDKSNNTAYLELARLTSEDSAIYYCARSDGNVGYVALDYWG	160	:	:
Db	76	TNGTYNYNEKPKSKATITVDKSSSTATNMQSSLISEDSANVYCARYGN----	130	SFDYWG	:
Qy	161	QGTITVTIVSSGGGGSGGGGGGGGDIELTQSPSILAVSLGORATISCRASESVDSYGDSF	220	:	:
Db	131	QGITVTIVS-----SRMDXEDIELTQSPDSLAVSLGORATISCRASESVDSYGNSF	180	:	:
Qy	221	MHWYQQRPQGPDKLLIYRASNLSEGVPARFSGSGESDFTLTIDPVEEDDAVVYCLQSM	280	:	:
Db	181	MQWYQQKFGPPKLLIYRASNLSEGIIPARFSGTGSRDTFTLTINPVEADDDVATYYCQSD	240	:	:
Qy	281	EDP--YTFGGGTGLEIKRAAASGGSGGGSGCG	310	:	:
Db	241	EYPWTYTFGGGTGLEIKR-----GSGSGNSRGK	268	:	:

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RESULT 3
US-09-419-788-30
; Sequence 30, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; TITLE OF INVENTION: Resistance
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
US-09-419-788-30
; OTHER INFORMATION: natural origin

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	Query Match	53.5%	Score 923;	DB 4;	Length 267;
	Best Local Similarity	71.7%;	Pred. No. 2.1e-58;		
	Matches 180;	Conservative 25;	Mismatches 42;	Indels 4;	Gaps 3
Qy	48	EVKLOQSGAEIVRGVSVKISKCSGYTFTDYGMSWKQSHAKSLIEWLIGLSTYYGDPST	107		
Db	1	EVKLOQSGAEIVKPGASVKISKASDYSFTGYNMNVKQSHGKSLIEWIGNINPPYVGSTSY	60		
Qy	108	NQRFKQKATMTVDKSSNTAYLELARTSEDSAIYYCARSDGNYGYYYALDYWGQGTITVTV	167		
Db	61	NQRFKQKATLTVDKSSSTAYNMQLSLTSEDSAAVYICA-VGNGYVDWFA--YWGQGTILTVTV	117		
Oy	168	SSGGGGSGGGSGGGGGDIETQSPSSIAVSLGQRATISCRASES-VDSYGDPSFMHWYQQ	226		

RESULT 2

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US-08-894-922A-10
; Sequence 10, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITELAM, Garry Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokullis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 60113/241261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-894-922A-10

FRAGME

US-09-419-788-30
; Sequence 30, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
; US-09-419-788-30

Query Match      53.5%; Score 923; DB 4; Length 267;
Best Local Similarity 71.7%; Pred.No. 2.le-58;
Matches 180; Conservative 25; Mismatches 42; Indels 4; Gaps 3

Qy      48 EVKLQQSGAELVPRPGSVKISKCGSYTFDYGMSSWVKSHAKSLIEWIGLIITYYGDPSY 107
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 EVKLQQSGAELVKPGASVKISCKASYDFTGYMMNMWVKQSHGKSLEWICNINPYGSTSY 60

Qy     108 NORPKGKATMTVDKSSNTAYLELARITSEDSALYYCARSDGNHYGYIYLDYVGOGTTVT 167
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     61 NORPKGKATLTVDKSSSTAYMQLNLSITSEDSAVYYCA--VGGNYVDWFDA--YWGQGFLVTV 117

Qy    168 SSGGGSGGGSGGGSDIELTQSPSSLVASLGLQRATISCRASES-VDSYGDSFMHWYQQ 228

```


APPLICANT: Iverson, Brent L.
APPLICANT: Georgiou, George
APPLICANT: Burks, Elizabeth A.
TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS
TITLE OF INVENTION: OF PROTEINS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,408
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,409
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSS:593
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/447-7577
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
US-09-070-408-132

Query Match 53.0%; Score 914; DB 3; Length 269;
Best Local Similarity 70.6%; Pred. No. 9.4e-58;
Matches 178; Conservative 30; Mismatches 40; Indels 4; Gaps 2;
QY 48 EVKLOQSGAELVRPGVSVKISCKGSGYFTFDYGMVWKQSHAKSLWIGLISYYGDPSY 107
DB 2 EVQLQSGPELVKPGASVLRMSCKSGYFTFDYVWVRQSHGKSLDIYGISYSGVTGY 61
QY 108 NORFKGKATMTVDKSSNTAYLELRLTSDSAIYYCARSDGNYYGYALDYWGQGTITV 167
DB 62 NQKFKGKATLTVDKSSSTAYMELRLTSDSAIYYCAGSSGN--KWAMDYWGHGASVTV 118
QY 168 SSGGGSGGGSGGGSGGSDIELTQSPSSLAVSLGORATISCRASES-VDSYGDSPFMHWYQ 226
DB 119 SSGGGSGGGSGGGSGGSDIYLTQTPSLPVSLSGDAQATISCRSSQSLVHSGNTYLNWY 178
QY 227 KPGQPPKLLIYRASNLGSGVPARFSGSGSDFTLTIDPVEEDAAVYYCLQSMEDPYTF 286
DB 179 KAGQSPKLLIYKVSNGFSGVPARFSGSGSDFTLTIDRVEEDAAIYYCSQTHVPPTF 238
QY 287 GGGTKLEIKRAA 298
DB 239 GSGTKLEIRAS 250

RESULT 7
US-09-423-439-32
Sequence 32, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32
Query Match 52.6%; Score 908; DB 3; Length 673;
Best Local Similarity 64.2%; Pred. No. 6.9e-57;
Matches 179; Conservative 35; Mismatches 45; Indels 20; Gaps 5;
QY 48 EVKLOQSGAELVRPGVSVKISCKGSGYFTFDYGMVWKQSHAKSLWIGLISYYGDPSY 107
DB 20 QVQLQPGAEVLKPGASVQLSCKASGYFTGYWIHWVKRPGQGLEWIGVNPSTGRSDY 79
QY 108 NORFKGKATMTVDKSSNTAYLELRLTSDSAIYYCARSDGNYYGYALDYWGQGTITV 167
DB 80 NEKFKNKATLTVDKSSSTAYMQLSSLTSDSAIYYCAR-ERAYGYDDAMDYWGQGTITV 138
QY 168 SSGGGSGGGSGGGSGGSDIELTQSPSSLAVSLGORATISCRASES--DSYGDSPFMHWYQ 225
DB 139 SSGGGSGGGSGGGSGGSDIELSQSPSSLAVSAGEKVTMSCKSSQSLNSRTRKNYLA 198
QY 226 QKPGQPPKLLIYRASNLGSGVPARFSGSGSDFTLTIDPVEEDAAVYYCLQSMEDPY- 284
DB 199 QRPQSPKLLIYWASTRTSGVDPDRFTGSGSGTDTLTLTSSVQAEADLAIIYCKOS---YT 254
QY 285 --TFGGTKLEIKRAASGGSGGGSGGGSGGGSGGGSG 321
DB 255 LRTFGGTKLEIKR-----GGGGSGGGSGGGSGGG 283
RESULT 8
US-08-403-853-18
Sequence 18, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:


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; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4

Query Match          50.6%; Score 873; DB 4; Length 353;
Best Local Similarity 58.7%; Pred. No. 1.1e-54;
Matches 168; Conservative 45; Mismatches 67; Indels 6; Gaps 3;

QY 16 QASKILILVAMWFGTTA-----EVSTARAAQPAMAEVKLQSGABELVRPGVSVKISCKG 71
Db 2 ETDTLWLLWLLVPGSTGDPYDVPDYDACAQPARSEIQQTGPELVKPGASVKISCKA 61

QY 72 SGYTFDYGMSWVKQSHAKSLEWIGLISYIGDPSNQRPKGKATMTVDKSSNTAYLELA 131
Db 62 SGYSFTDYIIFWVKQSHGKSLWTGNNNPYGSTYNLAKFKGKATLTVDKSSSTAYMQLN 121

QY 132 RLTSSEDAIYYCARSDGNYG-VYYALDYMGGTFTVSSGGGGGGGGGGGGSDIELTQ 190
Db 122 SLTSEDAVYICVRGVYVYSSYEAPYQGGTLTVSAGGGGGGGGGGGGGSDVVMTQ 181

QY 191 SPSSLAVSLGQATISCRASES-VDSYGDSFMHWYQQPKQPPLLIYRASNLSEGVPAR 249
Db 182 TPLTLITITIGQPASISCKSSQSLSDGKTYLWNLQRPQSPTRLJLYLVSKLDSGVPR 241

QY 250 FSGSGSEDTLTDVPEEDDAAYVYCLQSMEDPYTFGGGTKLEIK 295
Db 242 FTGSGSGDTFLKISRVEADLGIYCWGAHPQTFGGGTKLEIK 287

RESULT 11
US-09-526-738A-4
; Sequence 4, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526, 738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-4

Query Match          49.5%; Score 853.5; DB 4; Length 258;
Best Local Similarity 65.4%; Pred. No. 1.8e-53;
Matches 166; Conservative 29; Mismatches 48; Indels 11; Gaps 3;

QY 46 MAEVKLOQSGAELVRPGVSVKISCKSGYTFDYGMSWVKQSHAKSLEWIGLISYIGDP 105
Db 1 MAQVKLOQSGAELAKPGASVKMSCKTSGYTFTSYMNWVKQRPQCGGLEWIGYINPTGYT 60

QY 106 SYNQRFKGTATMTVDKSSNTAYLELARLTSEDAIYYCARSDGNYGYYYALDYWGQTTV 165
Db 61 KYNQFKDKATLTADKSSSTAYMQLSSLTNVDSAVYYCTT-----GYSY-FDYWGQTTV 114

QY 166 TVSSGGGGGGGGGGGGSDIELTQSPSSLAVSLGQATISCRASESVDSYGDSFMHWYQ 225
Db 115 TVSSGGGGGGGGGGGGSDIELTQSPAINSPASPEKVTITCSASSV-----NYMHWFO 169

QY 226 QKPGQPKLIYRASNLSEGVPARFSGSGSEDTLTDVPEEDDAAYVYCLQSMEDPYT 285
Db 170 QKPGTSPKLIWISSTNLASGVPARFSGSGSGTSLTISRMEADAATYYCQQRSSYPYT 229

QY 286 FGGGTKLEIKRAAA 299
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Query Match          49.0%; Score 844.5; DB 4; Length 256;
Best Local Similarity 65.1%; Pred. No. 7.9e-53;
Matches 164; Conservative 29; Mismatches 48; Indels 11; Gaps 3;

QY 48 EVKLOQSGAELVRPGVSVKISCKSGYTFDYGMSWVKQSHAKSLEWIGLISYIGDPSY 107
Db 1 QVKLOQSGAELAKPGASVKMSCKTSGYTFTSYMNWVKQRPQCGGLEWIGYINPTGYTKY 60

QY 108 NORFKGTATMTVDKSSNTAYLELARLTSEDAIYYCARSDGNYGYYYALDYWGQTTVTV 167
Db 61 NQKFKDKATLTADKSSSTAYMQLSSLTNVDSAVYYCTT-----GYSY-FDYWGQTTVTV 114

QY 168 SSGGGGGGGGGGGGGSDIELTQSPSSLAVSLGQATISCRASESVDSYGDSFMHWYQOK 227
Db 115 SSGGGGGGGGGGGGGSDIELTQSPAINSPASPEKVTITCSASSV-----NYMHWFOOK 169

QY 228 PQOPPKLIYRASNLSEGVPARFSGSGSEDTLTDVPEEDDAAYVYCLQSMEDPYTFG 287
Db 170 PGTSPKLIWISSTNLASGVPARFSGSGSGTSLTISRMEADAATYYCQQRSSYPYTFG 229

QY 288 GGTGLEIKRAAA 299
      |||||:|||||
Db 230 GGTGLEIKRAAA 241

RESULT 13
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTERBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESC
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 48.8%; Score 842; DB 2; Length 244;
Best Local Similarity 65.3%; Pred. No. 1.1e-52;
Matches 164; Conservative 32; Mismatches 45; Indels 10; Gaps 4;
QY 48 EVKLOQSGAELVRPGSVKISCKSGYFTDYGMSVVKSHAKSLEWIGLSTIYYGDPSTY 107
DB 1 EVLOQSGAELVKPGASVKLSKASGYFTTSHMHVVKORAGQLEWIGFNPNGRTNY 60
QY 108 NORFKGKATMTVDKSSNTAYLELRLTSEDAIYYCARSDGNY-GYYALDYWGQTTVT 166
DB 61 NFKFSKATLTVDKSSNTAYMQLSLTSEDAIYYCARSDYDGRYP--DYWGQTTVT 118
QY 167 VSSGG 226
DB 119 VSSGG 173
QY 227 KPGQPPKLLIYRASNLSEGVPAFSGSGSGSFTLTIDPVEDDAAVYYCLOSMEDP--Y 284
DB 174 KPGSPRLIYDTNLSAGVPRFSGSGSGTSLTISRMEADAATYYCQWSSYPMY 233
QY 285 TFGGGTKLEIK 295
DB 234 TFGGGTKLEIK 244

RESULT 14
US-08-553-497A-18
Sequence 18, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-18
Query Match 48.6%; Score 837.5; DB 2; Length 239;
Best Local Similarity 66.1%; Pred. No. 2.3e-52;
Matches 164; Conservative 34; Mismatches 35; Indels 15; Gaps 4;
QY 48 EVKLOQSGAELVRPGSVKISCKSGYFTDYGMSVVKSHAKSLEWIGLSTIYY 102
DB 1 EVKLOESGDLVKPGSLKLSAASGFTFSSYCMWVRQTPDKRLESVATISSGAYIY 60
QY 103 GDSYNQRFKATMTVDKSSNTAYLELRLTSEDAIYYCARSD-GNYGYVYALDYWGQ 161
DB 61 PD-----SVKGRFTISRDNAGNTLYLQMSLSKSEDTAMYYCARLETGD----YALDYWGQ 111
QY 162 GTTIVTSSGG 221
DB 112 GTTIVTSSGG 171
QY 222 HWYQKPGQPPKLLIYRASNLSEGVPAFSGSGSGSFTLTIDPVEDDAAVYYCLOSM 281
DB 172 HWYQKPGQPPKLLIYRASNLSEGVPAFSGSGSGTDFSLNHPVEDDIAVYFCQSRK 231
QY 282 DPTTFGGG 289
DB 232 VWSFGGG 239
RESULT 15
US-09-423-439-51
Sequence 51, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS

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;
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

Query Match      48.5%; Score 836.5; DB 3; Length 666;
Best Local Similarity 60.9%; Pred. No. 8.4e-52;
Matches 167; Conservative 26; Mismatches 64; Indels 17; Gaps 3;

QY 48 EVKLOQSGAELVRPGVSVKISKSGYTFDYGMVWVKQSHAKSLEWIGLITYYGDPSPY 107
DB 20 EVQLQSGAELVRSAGSVKLSCTASGFNIKONTYMHVVKORPEQGLEWIAWIDPENGDT 79
QY 108 NORFKGKATVVDKSNNTAYLELRLTSDSAIYYCARSDGNYYGYVALDYWGQGTITV 167
DB 80 APKFRGKATLTADSSNTAYLHLSLTSEDYVYCHVL--IYAGYLAMDYWGQGTSAV 137
QY 168 SSGGGSGGGSGGGSDIELTQSPSSLAVSLGQRATISCRASESVDSYGDSPMHVYQOK 227
DB 138 SSGGGSGGGSGGGSGGQIVLTQSPAIMSASPGKVTITCSASSV-----TYMHWFQOK 192
QY 228 PGQPPKLLIYRASNLESGVPAFPSGSGSDFTLTIDPVEEDDAVYVYCLQSMEDPYTFG 287
DB 193 PGTSPLKIWIYSTNLASGVPAFPSGSGGTSYSLTISRMEADAATYVYCOQRSTYPLTFG 252
QY 288 GGTKLEIKRAAASGGGGSGGGSGGGSGGGSGGGGS 321
DB 253 AGTKLEIKR-----GGGGSGGGSGGGSGGS 276
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Search completed: August 23, 2005, 11:29:18
Job time : 319 secs

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OM protein - protein search, using sw model

Run on: August 23, 2005, 11:29:22 ; Search time 1836 Seconds

(without alignments)

70.170 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNLRAGKVDQASKI.....GSGGGSGGGGASPVQFI 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	978	56.7	260	10	US-09-782-672-2
2	978	56.7	260	10	US-09-782-671B-2
3	978	56.7	260	11	US-09-813-444-2
4	957	55.5	762	20	US-11-035-599-28
5	947.5	54.9	252	14	US-10-169-351-49
6	935.5	54.2	239	9	US-09-808-037-6
7	935.5	54.2	239	14	US-10-162-889-6
8	935.5	54.2	239	15	US-10-384-788-6
9	935.5	54.2	239	15	US-10-618-856-6
10	935.5	54.2	239	17	US-10-749-522-6
11	935.5	54.2	239	20	US-11-073-526-6

12	932.5	54.1	248	17	US-10-879-994-14	Sequence 14, Appl
13	932.5	54.1	248	17	US-10-610-452-14	Sequence 14, Appl
14	927	53.7	261	16	US-10-689-008-24	Sequence 24, Appl
15	918	53.2	895	16	US-10-296-085A-19	Sequence 19, Appl
16	918	53.2	895	16	US-10-296-085A-20	Sequence 20, Appl
17	918	53.2	895	16	US-10-296-085A-27	Sequence 27, Appl
18	918	53.2	895	17	US-10-496-179-4	Sequence 4, Appl
19	918	53.2	896	16	US-10-296-085A-17	Sequence 17, Appl
20	918	53.2	896	16	US-10-296-085A-18	Sequence 18, Appl
21	918	53.2	896	16	US-10-296-085A-26	Sequence 26, Appl
22	918	53.2	896	17	US-10-496-179-3	Sequence 2, Appl
23	918	53.2	896	17	US-10-496-179-7	Sequence 3, Appl
24	918	53.2	899	16	US-10-496-179-5	Sequence 7, Appl
25	918	53.2	899	17	US-10-296-085A-28	Sequence 28, Appl
26	917.5	53.2	533	15	US-10-257-864A-96	Sequence 5, Appl
27	917.5	53.2	533	15	US-10-221-131-101	Sequence 96, Appl
28	917.5	53.2	533	15	US-10-399-518-125	Sequence 101, App
29	917.5	53.2	533	16	US-10-399-585-124	Sequence 125, App
30	917.5	53.2	533	16	US-10-645-085A-96	Sequence 124, App
31	917.5	53.2	507	15	US-10-239-656-47	Sequence 96, Appl
32	900.5	52.2	510	15	US-10-239-656-48	Sequence 47, Appl
33	893.5	51.8	510	15	US-10-239-656-49	Sequence 48, Appl
34	893.5	51.8	510	15	US-10-259-087A-18	Sequence 18, Appl
35	891.5	51.7	242	14	US-10-689-008-18	Sequence 18, Appl
36	891.5	51.7	242	16	US-11-036-098-18	Sequence 18, Appl
37	891.5	51.7	242	16	US-10-027-770-5	Sequence 5, Appl
38	888.5	51.5	269	13	US-10-114-716A-46	Sequence 46, Appl
39	887.5	51.4	264	14	US-10-930-548-46	Sequence 46, Appl
40	887.5	51.4	296	17	US-10-784-305-2	Sequence 2, Appl
41	883.5	51.2	274	15	US-10-257-864A-92	Sequence 92, Appl
42	883	51.2	274	16	US-10-645-085A-92	Sequence 92, Appl
43	883	51.2	269	13	US-10-027-770-2	Sequence 2, Appl
44	878.5	50.9	274	14	US-10-138-505-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-782-672-2

; Sequence 2, Application US/09782672

; Publication No. US20030036092A1

; GENERAL INFORMATION:

; APPLICANT: Iverson, Brent

; Chen, Gang

; Olsen, Mark J.

; Daugherty, Patrick S.

; TITLE OF INVENTION: Directed Evolution of Enzymes and

; Antibodies

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESS: ARNOLD, WHITE AND DURKEE

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/782,672

; FILING DATE: 12-Feb-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/847,063

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Highlander, Steven L.

```

;
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSB620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-672-2

Query Match          56.7%; Score 978; DB 10; Length 260;
Best Local Similarity 74.2%; Pred. No. 2.2e-56;
Matches 187; Conservative 30; Mismatches 31; Indels 4; Gaps 2;

QY 48 EVKLOQSGAELVRPGVSVKISCKSGYTFDTYGMVWVQSHGKSLDYIGVISYSGVTGY 107
Db 1 EVQLQSGPELVKPGASVRMSCKSGYIFDTFYMNVWVQSHGKSLDYIGVISYSGVTGY 60
QY 108 NQRFKGAATWVDKSNNTAYLELRLTSDSAIYYCARSDGNVGYYYALDYGQGTFTTV 167
Db 61 NQKFKGKATLTVDKSSSTAYMELRLSTSDSAVYYCAGSSGN---KWAMDYWGHGASVTV 117
QY 168 SSGGGSGGGGGGGGGDIETLQSPSLAVSLGORATISCRASES-VDSYGDSPFMHWYQQ 226
Db 118 SSGGGSGGGGGGGGGGGDIVLTQSPASLAVSLGORATISCRSSQSLVHSGNTYLNWYQQ 177
QY 227 KPGQPPKLLIYRASNLKESGVPARFSGSGSESDFTLTIDPVEEDDAVYYCLQSMEDPYTF 286
Db 178 KPGQPPKLLIYKVSNRFGVPARFSGSGSESDFTLTIDPVEEDDAIYYCSQTHVPPTF 237
QY 287 GGSTKLEIKRAA 298
Db 238 GSGTKLELKRAS 249

RESULT 2
US-09-782-671B-2
; Sequence 2, Application US/09782671B
; Publication No. US20030100023A1
; GENERAL INFORMATION:
; APPLICANT: IVERSON, BRENT
; APPLICANT: GEORGIU, GEORGE
; APPLICANT: CHEN, GANG
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION METHODS USING CELL
; FILE REFERENCE: MXGN:004USC2
; CURRENT APPLICATION NUMBER: US/09/782,671B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 09/084,141
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: 08/447,402
; PRIOR FILING DATE: 1995-05-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-782-671B-2

Query Match          56.7%; Score 978; DB 10; Length 260;
Best Local Similarity 74.2%; Pred. No. 2.2e-56;
Matches 187; Conservative 30; Mismatches 31; Indels 4; Gaps 2;

QY 48 EVKLOQSGAELVRPGVSVKISCKSGYTFDTYGMVWVQSHGKSLDYIGVISYSGVTGY 107
Db 1 EVQLQSGPELVKPGASVRMSCKSGYIFDTFYMNVWVQSHGKSLDYIGVISYSGVTGY 60
QY 108 NQRFKGAATWVDKSNNTAYLELRLTSDSAIYYCARSDGNVGYYYALDYGQGTFTTV 167
Db 61 NQKFKGKATLTVDKSSSTAYMELRLSTSDSAVYYCAGSSGN---KWAMDYWGHGASVTV 117
QY 168 SSGGGSGGGGGGGGGDIETLQSPSLAVSLGORATISCRASES-VDSYGDSPFMHWYQQ 226
Db 118 SSGGGSGGGGGGGGGGGDIVLTQSPASLAVSLGORATISCRSSQSLVHSGNTYLNWYQQ 177
QY 227 KPGQPPKLLIYRASNLKESGVPARFSGSGSESDFTLTIDPVEEDDAVYYCLQSMEDPYTF 286
Db 178 KPGQPPKLLIYKVSNRFGVPARFSGSGSESDFTLTIDPVEEDDAIYYCSQTHVPPTF 237
QY 287 GGSTKLEIKRAA 298
Db 238 GSGTKLELKRAS 249

RESULT 3
US-09-813-444-2
; Sequence 2, Application US/09813444
; Publication No. US20040072740A1
; GENERAL INFORMATION:
; APPLICANT: IVERSON, BRENT
; APPLICANT: GEORGIU, GEORGE
; APPLICANT: CHEN, GANG
; APPLICANT: OLSEN, MARK J.
; APPLICANT: DAUGHERTY, PATRICK S.
; TITLE OF INVENTION: Directed Evolution of Enzymes and Antibodies
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,444
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSB620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-813-444-2

Query Match          56.7%; Score 978; DB 11; Length 260;
Best Local Similarity 74.2%; Pred. No. 2.2e-56;
Matches 187; Conservative 30; Mismatches 31; Indels 4; Gaps 2;

QY 48 EVKLOQSGAELVRPGVSVKISCKSGYTFDTYGMVWVQSHGKSLDYIGVISYSGVTGY 107
Db 1 EVQLQSGPELVKPGASVRMSCKSGYIFDTFYMNVWVQSHGKSLDYIGVISYSGVTGY 60
QY 108 NQRFKGAATWVDKSNNTAYLELRLTSDSAIYYCARSDGNVGYYYALDYGQGTFTTV 167
Db 61 NQKFKGKATLTVDKSSSTAYMELRLSTSDSAVYYCAGSSGN---KWAMDYWGHGASVTV 117
QY 168 SSGGGSGGGGGGGGGDIETLQSPSLAVSLGORATISCRASES-VDSYGDSPFMHWYQQ 226
Db 118 SSGGGSGGGGGGGGGGGDIVLTQSPASLAVSLGORATISCRSSQSLVHSGNTYLNWYQQ 177
QY 227 KPGQPPKLLIYRASNLKESGVPARFSGSGSESDFTLTIDPVEEDDAVYYCLQSMEDPYTF 286
Db 178 KPGQPPKLLIYKVSNRFGVPARFSGSGSESDFTLTIDPVEEDDAIYYCSQTHVPPTF 237
QY 287 GGSTKLEIKRAA 298
Db 238 GSGTKLELKRAS 249
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Db 1 EVOLQSGPELVKPGASVRMSKSSGYIFTDFYMNWVRQSHKSLDYIGVISPVGVTGY 60
Qy 108 NQRFKGTATWTVKSSNTAYLEARLTSEDSAIYYCARSDGNYGYVALDYWGQGTFTV 167
Db 61 NQRFKGTATWTVKSSNTAYMELRSLTSEDSAVYYCAGSSGN---KWMDYWGHSVTV 117
Qy 168 SSGGGSGGGGGGGSDIELTQSPSLAVSLGQRATISCRASES-VDSYGDSPFMHWYQQ 226
Db 118 SSGGGSGGGGGGGSDIVLTQSPASLAVSLGQRATISCRSQSLVHSGNTLYLNWYQQ 177
Qy 227 KPGQPPKLLIYRASNLSESGVPAFSGSGSDEFTLTIDPVEEDAAVYYCLQSMEDPYTF 286
Db 178 KPGQPPKLLIYKYNRPSGVPARFSGSGSDEFTLTIDPVEEDAAIYYCSQTHVPPTF 237
Qy 287 GGGTKLEIKRAA 298
Db 238 GSGTKLEIKRAS 249

RESULT 4
US-11-035-599-28
; Sequence 28, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Fandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-28

Query Match 55.5%; Score 957; DB 20; Length 762;
Best Local Similarity 72.1%; Pred. No. 1.5e-54;
Matches 186; Conservative 22; Mismatches 46; Indels 4; Gaps 1;

Qy 39 ARAAQPAEAELVKLOQSGAELVRPGVSKICKSGYTFDTYGMVWQSHAKSLEWIGLI 98
Db 24 ARGADAGAEVVKLOQSGAELMKPGASVKICKATGYTFSSYIEWYKQRPQGHGLEWIGE 83
Qy 99 STYIGDPSYNQRFKGTATWTVKSSNTAYLEARLTSEDSAIYYCARSDGNYGYVALDY 158
Db 84 LPSSGSGTNYNEKFKGATFTADTFSTAYWQLSSLTSEDSAVYYCARFDG----YLPFDH 139
Qy 159 WGQGTFTTVSSGGGGGGGGSDIELTQSPSLAVSLGQRATISCRASESVDSYGD 218
Db 140 WGQGTFTTVSSGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASKSVITSGV 199
Qy 219 SFMHWYQKPGQPPKLLIYRASNLSESGVPAFSGSGSDEFTLTIDPVEEDAAVYYCLQ 278
Db 200 SYMHWYQKPGQPPQLLIYASNLSESGVPAFSGSGSGTDTLTINHPVEEDAAIYYCHH 259
Qy 279 SMEDPYTFGGTKLEIKR 296
Db 260 SRELPRTFGGTKLEIKR 277

RESULT 5
US-10-169-351-49
; Sequence 49, Application US/10169351
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; Publication No. US20030157090A1
; GENERAL INFORMATION:
; APPLICANT: BENVENUTO, EUGENIO
; APPLICANT: FRANCONI, ROSELLA
; APPLICANT: DESIDERIO, ANGIOLA
; APPLICANT: TAVLADORAKI, PARASKEVI
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
; TITLE OF INVENTION: WHICH INCLUDE THEM
; FILE REFERENCE: 4161-4
; CURRENT APPLICATION NUMBER: US/10/169,351
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/IT00/00554
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: IT RM99A000803
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv (F8)
; OTHER INFORMATION: amino acid sequence
US-10-169-351-49

Query Match 54.9%; Score 947.5; DB 14; Length 252;
Best Local Similarity 71.1%; Pred. No. 2.1e-54;
Matches 180; Conservative 29; Mismatches 39; Indels 5; Gaps 2;

Qy 48 EVKLQSGAELVRPGVSKICKSGYTFDTYGMVWQSHAKSLEWIGLIITYYGDPSY 107
Db 1 QVQLQESGGDLVQPGGSLKSLCAASGFTFSYSGMSWVRQTPDKRLVATINSNGSTFY 60
Qy 108 NQRFKGTATWTVKSSNTAYLEARLTSEDSAIYYCARSDGNYGYVA----LDYWGQGT 163
Db 61 PDSVKGRFTISRDNKNTLYLQWSSLKSEDTAMYICARR-RNYPYYGSRGYFDYWGQGT 119
Qy 164 TVTVSSGGGGGGGGGGSDIELTQSPSSLAIVSLGQRATISCRASESVDSYGDSPFMHW 223
Db 120 TVTVSSGGGGGGGGGGSDIELTQSPASLAVSLGQRATISCRASESVDSYGNFPMHW 179
Qy 224 YQKPGQPPKLLIYRASNLSESGVPAFSGSGSDEFTLTIDPVEEDAAVYYCLQSMEDP 283
Db 180 YQKPGQPPKLLIYRALNLESGIPARFSGSGSRTDFTLTINPVEADDAVYYCQSNEDP 239
Qy 284 YTFGGTKLEIKR 296
Db 240 WTFGGTKLEIKR 252

RESULT 6
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Bilal
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 248
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-610-452-14

Query Match          54.1%; Score 932.5; DB 17; Length 248;
Best Local Similarity 72.0%; Pred. No. 2e-53;
Matches 180; Conservative 26; Mismatches 41; Indels 3; Gaps 2;

QY 48 EVKLOQSGAELVRPGVSVKISCKGSGYTTFTDYGMSVVKSHAKSLEWIGLISYYGDPSTV 107
Db 1 QVLOQSGAELAKPGASVKNMSCKASGYTFTSTMHWIKORPCQGLEWIGIYNPSTGYTEY 60

QY 108 NORFKGKATMTVDKSSNTAYLELARLTSDSDSAIYYCARSDGNYYYYALDYWGQGTFTV 167
Db 61 NQKFKDKATLTADKSSSTAYMQLSSLTSDSDSAVYYCARD--VYDEDVMDYWGQGTSTNV 118

QY 168 SS-GGGSGGGSGGGGGSDIELTQSPSSLAIVSLGQATATISCRASESVDSYGSFMHWYQQ 226
Db 119 SSAGGGSGGGSGGGGGSDIVLTQSPASLAIVSLGQATATISCRASESVDFGGSFMNWFQQ 178

QY 227 KPGQPPKLLIYRASNLNLESGVPARFSGSGSESDFTLTIDPVEEDDAAVYYCLOSMEDPYTF 286
Db 179 KPGQPPKLLIYAASNOGSGVPARFSGSGSGTDFSLNIHPMEGDAAMYFCQIKEYPTWF 238

QY 287 GGGTKLEIKR 296
Db 239 GGGTKLEIKR 248

RESULT 14
US-10-689-006-24
; Sequence 24, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 261
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: nucleic acid encoding scFv antibody 10A
US-10-689-006-24

Query Match          53.7%; Score 927; DB 16; Length 261;
Best Local Similarity 70.1%; Pred. No. 4.8e-53;
Matches 178; Conservative 23; Mismatches 45; Indels 8; Gaps 2;

QY 46 MAEVLKQSGAELVRPGVSVKISCKGSGYTTFTDYGMSVVKQSHAKSLEWIGLISYYGDP 105
Db 1 MAQVKLQSGPELVKPGASVKNMSCKASGYTFTSYVMHWVKQSGKSLWIGITIDPYGGT 60

QY 106 SYNQRKPKATMTVDKSSNTAYLELARLTSDSDSAIYYCARSDGNYYYYALDYWGQGTTV 165
Db 61 SYNQKPKGKATLTVDKSSSTAYIQLKSLTSDSDSAVYYCARWD---GYGGFSYWGQGTWV 117

QY 166 TVSSGGGGSGGGSGGGGGSDIELTQSPSSLAIVSLGQATATISCRASESVDSYGSFMHWYQ 225

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 12:27:22 ; Search time 1940 Seconds

(without alignments)
4046.134 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNRSAGKVDQASKI.....GSGGGGGGGGASPVQFI 329

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blolsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1725	100.0	1030	6 AX111694	AX111694 Sequence
2	1239	71.8	990	6 AX111696	AX111696 Sequence
3	1202.5	69.7	946	6 AX111697	AX111697 Sequence
4	1186.5	68.8	927	6 AX111695	AX111695 Sequence

5	1045.5	60.6	1632	12 SYN507107	AJ507107 Synthetic
6	1035.5	60.0	1695	12 SCO544530	AJ544530 Synthetic
7	1034	59.9	900	12 AY710431	AY710431 Synthetic
8	1009	58.5	687	12 AF003707	AF003707 Synthetic
9	1004	58.2	906	6 AX111698	AX111698 Synthetic
10	1001	58.0	744	12 AF402256	AF402256 Synthetic
11	993.5	57.6	2190	6 AX100186	AX100186 Synthetic
12	992.5	57.5	876	6 AX100194	AX100194 Sequence
13	992.5	57.5	969	6 AX100188	AX100188 Sequence
14	991	57.4	687	12 AF003705	AF003705 Synthetic
15	991	57.4	897	6 CO881538	CO881538 Sequence
16	991	57.4	1698	6 BD206134	BD206134 Polyvalen
17	991	57.4	1698	6 AX011206	AX011206 Sequence
18	986	57.2	4354	12 ASY14583	Y14583 Artificial
19	983	57.0	925	6 E30617	E30617 Antibody an
20	980	56.8	1010	6 AR126374	AR126374 Sequence
21	978	56.7	780	6 AR031393	AR031393 Sequence
22	976.5	56.6	1817	6 AX739887	AX739887 Sequence
23	948.5	55.0	1906	6 AX777477	AX777477 Sequence
24	947.5	54.9	756	6 AX164036	AX164036 Sequence
25	946.5	54.9	891	6 AS6705	AS6705 Sequence 9
26	946	54.8	882	12 SCO278109	SCO278109 Synthetic
27	942.5	54.6	795	10 MMSCFVP25	MMSCFVP25 Artificial
28	935.5	54.2	717	6 AR482235	AR482235 Sequence
29	935	54.2	996	6 AS6700	AS6700 Sequence 4
30	935	54.2	896	6 AR343612	AR343612 Sequence
31	931	54.0	864	12 AY605056	AY605056 Synthetic
32	924	53.6	993	6 AX798477	AX798477 Sequence
33	924	53.6	2199	6 AX100182	AX100182 Sequence
34	923	53.5	888	6 AX100192	AX100192 Sequence
35	922.5	53.5	2214	6 CO856165	CO856165 Sequence
36	920	53.3	1725	6 AX001509	AX001509 Sequence
37	919	53.3	578	6 AX100184	AX100184 Sequence
38	918.5	53.2	894	6 AR316970	AR316970 Sequence
39	918	53.2	2952	6 AX306590	AX306590 Sequence
40	917.5	53.2	1605	6 BD169233	BD169233 Degraded
41	917.5	53.2	1605	6 BD169344	BD169344 Small rem
42	917.5	53.2	1605	6 BD102019	BD102019 Agonist a
43	917.5	53.2	1605	6 BD102173	BD102173 Apoptosis
44	916.5	53.1	797	6 AS6709	AS6709 Sequence 13
45	916	53.1	2691	6 AX306662	AX306662 Sequence

ALIGNMENTS

RESULT 1	AX111694	Sequence 1 from Patent WO0125415.	1030 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX111694					
DEFINITION	AX111694					
ACCESSION	AX111694					
VERSION	AX111694.1	GI:13927959				
KEYWORDS						
SOURCE		synthetic construct				
ORGANISM		other sequences; artificial sequences.				
REFERENCE						
AUTHORS		Cichutek, K. and Engelstaedter, M.				
TITLE		Gene transfer in human lymphocytes using retroviral scfv cell targeting				
JOURNAL		Patent: WO 0125415-A 1 12-APR-2001;				
FEATURES		Bundesrepublik Deutschland LET (DE)				
source		Location/Qualifiers				
		1. .1030				
		/organism="synthetic construct"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:32630"				
		/note="scFv kodierende Sequenz"				
ORIGIN						
Alignment Scores:		8.44e-118	Length:			1030
Pred. No.:		1725.00	Matches:			329
Score:		100.00%	Conservative:			0

Best Local Similarity: 100.00%		Mismatches: 0
Query Match: 100.00%		Indels: 0
DB: 6		Gaps: 0
US-10-089-278-6 (1-329) x AX111694 (1-1030)		
QY	1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyValAspGlnAlaSerLysIle 20	
DB	44 ATGGACTGTCACCAACCTCCGATCCGCTGAGGTAAAGTTGACCGAGCGCAAAATC 103	
QY	21 LeuIleLeuValAlaTrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40	
DB	104 CTAATTCCTCTGTGGCTTGGTGGGGTTTGGACCACTGCCAAAGTTCCGATGCCCGA 163	
QY	41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerClyAlaGluLeuValArg 60	
DB	164 GCGGCCACCGCGCCATGCGCGAGGTCAAGCTGCAGCAGTCAGCGGCTGAGCTGGGAGG 223	
QY	61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80	
DB	224 CTTGGGGTCTCAGTGAAGATTCTCGAAGGTTCTGGCTACACATTCAGTATATGGT 283	
QY	81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100	
DB	284 ATGAGCTGGGTGAAACAGAGTCATGCAAGAGTCTAGAGTGGATTGGACTTATTAGTACT 343	
QY	101 TyrTyrClyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120	
DB	344 TACTATGGGTGATCCTAGTTACACACAGAGGTTCAAGGGCAAGCCCAATGACTGTAGAC 403	
QY	121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140	
DB	404 AATCTCTCCACACAGCCTATTGGAACTTGCCAGACTGCACATCTCAGGATCTGCCATT 463	
QY	141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160	
DB	464 TATTATTGTGCAAGATCGGATGTAATTACGGGTATTACTATGCTTTGGACTACTGGGC 523	
QY	161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180	
DB	524 CAAGGCACATACGGTCCCGTCTCCTCAGGTGGAGCGGTTGAGCGGAGGTGGCTCTGGC 583	
QY	181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200	
DB	584 GGTGGCGGATCGGATATCGAGCTCACTCAGTCTCCATCTCTTTGGCTGTCTCTAGGG 643	
QY	201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220	
DB	644 CAGAGGGCCACCATATCTCTGCAGAGCCAGTGAAGTGTGATAGTTATGGCGATAGTTT 703	
QY	221 MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240	
DB	704 ATGCATCTGGTATCAGAGAAACAGGACAGCCACCACTCTCATCTATCTGTGATCC 763	
QY	241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260	
DB	764 AACCTAGATCTGGATCCCTCGCAGGTTCAGTGGCAGTGGCTCTGATCAGACTTCAC 823	
QY	261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280	
DB	824 CTCACCATCGATCTGTGGAGGAAGATGATGCTGCAGTGTATTACTGTCTGCAGAGTATG 883	
QY	281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAlaSer 300	
DB	884 GAGATCCGTACAGTTCGGAGGGGGACCAAGCTGGAAATAAACAAGCGGCGCGCATCG 943	
QY	301 GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly 320	
DB	944 GGCTCCGGGGCGGTGTTCTGGTGGTGTCTGGTGGTGTGGTCTGGTGGTGGTGGT 1003	
QY	321 SerGlyAlaSerProValGlnPheIle 329	
DB	1004 TCTGGGCGCAGCCAGTCCAGTTTATC 1030	

RESULT 2	AX111696	Sequence 3 from Patent WO0125415.	990 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX111696	AX111696				
DEFINITION	AX111696	AX111696				
ACCESSION	AX111696	AX111696				
VERSION	AX111696.1	GI:13927961				
KEYWORDS		synthetic construct				
SOURCE		other sequences; artificial sequences.				
ORGANISM		1 Cichutek,K. and Engelstaedter,M.				
REFERENCE		Gene transfer in human lymphocytes using retroviral scfv cell				
AUTHORS		targeting				
TITLE		Patent: WO 0125415-A 3 12-APR-2001;				
JOURNAL		Bundesrepublik Deutschland LfT (DE)				
FEATURES		Location/Qualifiers				
source		1..990				
		/organism="synthetic construct"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:32630"				
		/note="scfv kodierende Sequenz"				
ORIGIN						
Alignment Scores:						
Pred. No.:	3.96e-82	Length:	990			
Score:	1239.00	Matches:	243			
Percent Similarity:	82.23%	Conservative:	30			
Best Local Similarity:	73.19%	Mismatches:	45			
Query Match:	71.83%	Indels:	14			
DB:	6	Gaps:	5			
US-10-089-278-6 (1-329) x AX111696 (1-990)						
QY	1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysIle 20					
DB	1 ATGGACTGTCACCAACCTCCGATCCGCTGAGGTAAAGTTGACCGAGCGCAAAATC 60					
QY	21 LeuIleLeuValAlaTrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40					
DB	61 CTAATTCCTCTGTGGCTTGGTGGGGTTTGGACCACTGCCAAAGTTTTCGACTGCCGA 120					
QY	41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60					
DB	121 GCGGCCACCGCCCATGCCCCAGGTGCAGTGCAGCAGTCTGGGACTGAACTGGCAACA 180					
QY	61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80					
DB	181 CTTGGGGCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACGCCCTTTACTACTACTGG 240					
QY	81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIle----- 98					
DB	241 ATGCATCTGGTAAACAGAGGCTGCAGAGGCTCTGGATGGATTGGATGATACATTAATCCT 300					
QY	99 SerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThr 118					
DB	301 ACCACTGATTATACTGAC-----TACATCTGAAGTTCAAGGACAAGGCCACATTGACT 354					
QY	119 ValAspLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSer 138					
DB	355 GCAGACAAATCTCTCCAGTACAGCTACATGCACTGAGCAGCAGCTCATCTGAGGACTCT 414					
QY	139 AlaIleTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyr 158					
DB	415 GCAGCTTATTACTGTGCAAGATCG-----GGTGGTCTCTATGCTATGGACTAC 462					
QY	159 TrpGlyGlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGly 178					
DB	463 TGGGGGCAAGGGACCAACCGTCCACATCTCTCAGGTGGAGCGGTTTCAGCGGAGGTGC 522					
QY	179 SerGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSer 198					

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Db      523  TCTGGCGGTGGCGGATCGGACATCGAGTCTCAGTCTCCAGCAATCATGTCTGCATCT 582
Qy      199  LeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrglyAsp 218
Db      583  CCAGGGGAGAGGTCCACCAATACCTGAGTCCAGGTCACAGTGTA----- 627
Qy      219  SerPheMetHisTrpTyrglnGlnLysProGlyGlnProProLysLeuLeuIleTyrg 238
Db      628  AGTTACATGCACTGGTTCACAGCAGACCGACGACTTCTCCAAACTCTGGATTTATAGC 687
Qy      239  AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
Db      688  ACATCAACACCTGGCTTCTGAGTCCCTGCTCGTTCAGTGGCAGTGGATCTGGGACCTCT 747
Qy      259  PheThrLeuThrIleAspProValGluGluAspAlaValTyrglyCysLeuGln 278
Db      748  TACTCTCTCAATCAGCCGAATGGAGGCTGAAGATGCTGCCACTTATTATCTCCAGCAA 807
Qy      279  SerMetGluAspProTyrglyThrPheGlyGlyThrLysLeuGluLeuLysArgAlaAla 298
Db      808  AGGAGTAGTTACCATTCAGTTCGGCTCGGGCACCAGCTGGANATCAACCGGGCGGCC 867
Qy      299  AlaSerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlySerGly 317
Db      868  GCATCGGGCTCCGGGGCGGTGTTCTGGTGGTGGTCTGGTGGTGGTGGTCTGGT 927
Qy      318  GlyGlyGlySerGlyAlaSerProValGlnPheIle 329
Db      928  GGTGGTGGTCTGGCGCCAGCCAGTCCAGTTTATC 963

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RESULT 3

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AX111697
LOCUS      AX111697
DEFINITION Sequence 4 from Patent WO0125415.
ACCESSION AX111697
VERSION   AX111697.1
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.

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REFERENCE 1
AUTHORS   Cichutek, K. and Engelstaedter, M.
TITLE     Gene transfer in human lymphocytes using retroviral scfv cell

```

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JOURNAL   targeting

```

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Patent: WO 0125415-A 4 12-APR-2001;
Bundesrepublik Deutschland LET (DE)

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FEATURES
Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/notes="scfv kodierende Sequenz"

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ORIGIN

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Pred. No.: 1.8e-79 Length: 946
Score: 1202.50 Matches: 236
Percent Similarity: 83.12% Conservative: 30
Best Local Similarity: 73.75% Mismatches: 47
Query Match: 69.71% Indels: 7
DB: 6 Gaps: 4

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US-10-089-278-6 (1-329) x AX111697 (1-946)

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Qy      1  MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysile 20

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Db      1  ATGGACTGTCTCACCACCTCCGATCCGCTGAGGGTAAAGTTTACCCAGGCGGACAAATC 60

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Qy      21  LeuIleLeuValAlaThrPheGlyThrAlaGluValSerThrAlaArg 40

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Db      61  CTAATTCTCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120

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Qy      41  AlaAlaGlnProAlaMetAlaGluValLysLeuGlnLysSerGlyAlaGluLeuValArg 60

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Db      121  GCAGCCAGCGCGCCATGCGCGAGGTCAGTCTCAGCAGCATCGAGGCTGAGCTGGTGGG 180
Qy      61  ProGlyValSerValLysIleSerCysLysGlySerGlyTyrglyThrPheThrAspTyrgly 80
Db      181  CTTGGAGCTTCACTGAAGTGTCTCTGCAAGACTTCTGGCTTCTCTTCCACAGCTACTGG 240
Qy      81  MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db      241  ATGAACCTGGGTGAAGCTTGAGCCCTGAGCAAGGCTTGTAGTGGATTTGCATGATTCATCCT 300
Qy      101  TyrglyAspProSerTyrglyAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db      301  TCCGATAGTGAACACTAGTTAACTCAGAGGTTCAAGGACAAGCCACACTGACTGTAGAC 360
Qy      121  LysSerSerAsnThrAlaTyrglyLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db      361  AATCTCTCCAGCAGCAGCTACATGCAACTCAGCAGCCGACATCTGAGGACTCTGCGGTC 420
Qy      141  TyrglyCysAlaArgSer---AspGlyAsnTyrglyTyrglyTyrglyAlaLeuAspTyrgly 159
Db      421  TATTACTGTGCAAGATCTCTTTATGTAACCTACCCCTCTGGTTTACT-----TACTGG 474
Qy      160  GlyGlnGlyThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlyGlySer 179
Db      475  GGCCAGGACCAACGCTCAGCTCTCTCAGTGGAGCGGTTTCAGGCGGAGGTGGTCTCT 534
Qy      180  GlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerSerLeuAlaValSerLeu 199
Db      535  GCGGTGGCGGATCGGACATCGAGTCTCAGTCTCCAACCAACCATGGTGGTGGTGGTGGT 594
Qy      200  GlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrglyAspSer 219
Db      595  GGGGAGAAATCACTATCATCCTGAGTGGCAGCTCAAGTATATAAGTTTCC-----AAT 645
Qy      220  PheMetHisTrpTyrglnGlnLysProGlyGlnProProLysLeuLeuIleTyrglyAla 239
Db      646  TACTTGCATGGTATCAGCAGAACCGAGATCTCCCTAACTCTTGATTTATAGGACA 705
Qy      240  SerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPhe 259
Db      706  TCCAATCTGGCTTCTGGAGTCCAGCTCGCTTCACTGGCAGTGGTCTGGGACCTCTTAC 765
Qy      260  ThrLeuThrIleAspProValGluGluAspAlaValTyrglyCysLeuGlnSer 279
Db      766  TCTCTCACAATTGGCACCACCATGGAGCTGAAGATGTTGCCACTTACTTCTGCGGAGGGT 825
Qy      280  MetGluAspProTyrglyThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaAla 299
Db      826  AGTAGTATACCGTACACGTTCCGAGGGGGGAGCCACAGCTGGAAATAAAGCGGGCGCGCA 885
Qy      300  SerGlySerGlyGlyGlyGlySer---GlyGlyGlySerGlyGlyGlyGlySerGlyGly 318
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RESULT 4

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AX111695
LOCUS      AX111695
DEFINITION Sequence 2 from Patent WO0125415.
ACCESSION AX111695
VERSION   AX111695.1
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.

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REFERENCE 1
AUTHORS   Cichutek, K. and Engelstaedter, M.
TITLE     Gene transfer in human lymphocytes using retroviral scfv cell

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JOURNAL   targeting

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Patent: WO 0125415-A 2 12-APR-2001;
Bundesrepublik Deutschland LET (DE)

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FEATURES
Location/Qualifiers

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Pred. No.: 2 63e-78 Length: 927  
Score: 1186.50 Matches: 229  
Percent Similarity: 79.69% Conservative: 26  
Best Local Similarity: 71.56% Mismatches: 54  
Query Match: 68.78% Indels: 11  
DB: 6 Gaps: 2  
  
US-10-089-278-6 (1-329) x AX111695 (1-927)  
  
QY 1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyValAspGlnAlaSerLysIle 20  
DB 1 ATGGACTGTCTCACCACCTCCGATCCGCTGAGGTTAAAGTTGACCGAGCGAGCAAAATC 60  
  
QY 21 LeuIleLeuValAlaTTPTrpGlyPheGlyThrAlaGluValSerThrAlaArg 40  
DB 61 CTAATTTCTCTGTGGCTTGGTGGGGTTGGGACCACTGCCGAAGTTGCACTGCCCGA 120  
  
QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60  
DB 121 GCGGCCCGCCGCGCATGGCCGAGGTCAGCTCAGAGTCAGGACTGNACTTGTGAAG 180  
  
QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyThrPheThrAspTyrGly 80  
DB 181 CCTGGGGTTCAGTGAATCTGCTTGCAGGCTTCTGGCTACACCTTACCAGCTACTGG 240  
  
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100  
DB 241 ATGCACCTGGTGAAGCAGAGCGCTCGACCAAGCGCTTGAAGTGGATCGAGAGATTGATCCT 300  
  
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120  
DB 301 GTTGATAGTTATCTACTACATCAAACTTCAAGGCCAAGCCACACTGACTGTAGAC 360  
  
QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140  
DB 361 AAGTCTCTCCACCACAGCTACATGCACCTCAGCAGCTGACATCTCAGGACTCTGGCGTC 420  
  
QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160  
DB 421 TATTACTGTGCAGAAAGGCG-----TATGCTATGGACTACTGGGCG 462  
  
QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180  
DB 463 CAAGGACCAACCTCACCGTCTCTCAGGTGGATGCGGTTTCAGCGGAGGTGACTCTGGC 522  
  
QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200  
DB 523 GGTGGGGGATCGGACATCGAGCTCACTCAGTCACCAAGCAATCATGCTGCACTCTCCAGG 582  
  
QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220  
DB 583 GAGAAGGTCAACCATGCTCGATGCTGCGAGTCAAGTATA-----AGTTAC 627  
  
QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240  
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QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260  
DB 688 AAACCTGGCTTCTCGAGTCCCTGCTGCTCAGTGGCAGTGGGCTCTGGACCTCTATTCT 747  
  
QY 261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280  
DB 748 CTCCCAATCAGCAGCAGTGAAGGCTGAAGATGCTGCCACTTATTACTGCCATCGGAGT 807  
  
QY 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaSer 300
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DB 868 GGCTCCGGGGGGTGGTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTTGTTGTT 927  
  
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SYN507107 1632 bp RNA linear SYN 02-SEP-2002  
LOCUS  
DEFINITION  
Synthetic construct for anti-CD28 and anti-HMWG ScFv antibody,  
clone r28M.  
ACCESSION  
AJ507107  
VERSION  
AJ507107.1 GI:22759563  
KEYWORDS  
antibody; heavy chain; immunoglobulin; light chain; ScFv; variable  
region.  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
Grosse-Hovest L.  
Produktion und Charakterisierung supra-agonistischer bispezifischer  
CD28-Antikörper zur Tumor-Immuntherapie  
Thesis (2002) Department of Biology, University of Tuebingen,  
Tuebingen, Germany  
2 (bases 1 to 1632)  
Grosse-Hovest L.  
Direct Submission  
Submitted (28-AUG-2002) Grosse-Hovest L., Membrane Biochemistry,  
Max-Planck-Institute for Biochemistry, Am Klopferspitz 18a, 82152  
Martinsried, GERMANY  
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Score: 1045.50 Matches: 205
Percent Similarity: 80.99% Conservative: 25
Best Local Similarity: 72.18% Mismatches: 41
Query Match: 60.61% Indels: 13
DB: 12 Gaps: 3

US-10-089-278-6 (1-329) x SYN507107 (1-1632)

QY 27 TrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArgAlaAlaGlnProAlaMet 46
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QY 47 -----AlaGluValIysLeuGlnInSerGlyAla 56
Db 823 TTCCCTCCCTGGCACCTCTCTCAGGCTCTGGCGAGGTGAATCTGCAGCAGTCTGGACCT 882
QY 57 GluLeuValArgProGlyValSerValIleSerCysIysGlySerGlyThrPhe 76
Db 883 GAGCTGGTGAAGCTCTGGGCTCAGTGAAGATTCTCTGCAAGAGCTTCTGGCTACGCATTC 942
QY 77 ThrAspTyrGlyMetSerTrpValIysGlnSerHisAlaLysSerLeuGluTrpIleGly 96
Db 943 AGTAGGCTCTGGATGAAGTGGGTGAAGCAGAGCGCTGGCAGAGGTCTTGAGTGATGGA 1002
QY 97 LeuIleSerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThr 116
Db 1003 CGGATTATTCTCGAGATGGAGATACTAATAATGGGAAGTTCAAGGGCAAGGCCACA 1062
QY 117 MetThrValAspLysSerSerAnthrAlaTyrLeuGluLeuAlaArgLeuThrSerGlu 136
Db 1063 CTGACTGCAGACAAATCTCTCCAGCAGACGCTACATGAGCTCAGCAGCCTCTGTG 1122
QY 137 AspSerAlaIleTyrTyrCysAlaAspSerAspGlyAsnTyrGlyTyrTyr---TyrAla 155
Db 1123 GACTCTGGGCTATTCTCTGTGCAAG-----GGGAATACGGTAGTAGTTCCTATACT 1176
QY 156 LeuAspTyrTrpGlyGlnGlyThrThrValThrValSerSerGlyGlyGlySerGly 175
Db 1177 ATGGACTACTGGGGCCCAAGGACCAACCGTCAACGCTCTCTCAGTGGAGCGGTTCAAGC 1236
QY 176 GlyGlyGlySerGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeu 195
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QY 196 AlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSer 215
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QY 216 TyrGlyAspSerPheMetHisTrrTyrGlnGlnLysProGlyGlnProPolysLeuLeu 235
Db 1357 TATGGCAATAGTTTTATGCACTGTACCAAGCAGACAGAAACCAAGCAGACCACTCTCTC 1416

QY 236 IleTyrArgAlaSerAnLeuGluSerGlyValProAlaArgPheSerGlySerGlySer 255
Db 1417 ATCTATCTTGCATCCCAACCTAGAACTCTGGGTCCTCCAGGTTCTAGTGGCAGTGGATCT 1476
QY 256 GluSerAspPheThrLeuThrIleAspProValIcGluAspAlaAlaValTyrTyr 275
Db 1477 AGGACAGACTTCCACCTCACCATTGATCTGTGGAGCTGATGCTGCAACCTATTAC 1536
QY 276 CysLeuGlnSerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLys 295
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QY 296 AtcAlaAlaAla 299
Db 1597 CGGGCGCGCGCA 1608
RESULT 6
LOCUS SC0544530 1695 bp RNA linear SYN 12-MAR-2003
DEFINITION Synthetic construct for anti-CD95 and anti-HMWG scFv antibody,
clone r95M.
ACCESSION AJ544530
VERSION AJ544530.1 GI:28804184
KEYWORDS antibody; heavy chain; immunoglobulin; light chain; scFv; variable
region.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1695)
AUTHORS Grose-Hovest L.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2003) Grose-Hovest L., Immunology, University of
Tuebingen, Auf der Morgenstelle 15, 72076 Tuebingen, GERMANY
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GSVKVSKASGVTFTSYMMQVKAPGQGLEWIGFIDPSDSTYNQKFKGKATLT
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ORIGIN

Alignment Scores:
 Pred. No.: 4,01e-67 Length: 900
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 Percent Similarity: 87.60% Conservative: 25
 Best Local Similarity: 77.60% Mismatches: 31
 Query Match: 59.94% Indels: 0
 DB: 12 Gaps: 0

US-10-089-278-6 (1-329) x AY10431 (1-900)

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 Qy 67 IleSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGln 86
 Db 130 ATTAGTTGCAAGCTAGTGGTTATGCTTTTAGCCGTTATTGGATGAATGGGTTAAACAA 189
 Qy 87 SerHisAlaLysLeuSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSer 106
 Db 190 AGGCCTGGTCAAGACTCGAATGGATGGTCAATCTACCCGTGAGATGGAGATAATAAT 249
 Qy 107 TyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAla 126
 Db 250 TACAATGAAAGTTTAAAGGAAAGTGCACCTTACAGCTGATAAAAGTTCAAGTACCGCT 309
 Qy 127 TyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSer 146
 Db 310 TACATGCAATATCATCTCTACTAGTAGGAGATAGTCCGCTGACTTTTGTGCTAGATTT 369
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 Db 370 TATGGAAGTTCAAGTATATTTCCCTATGGATTATTTGGGACNAGGAACAAGTTTACA 429
 Qy 167 ValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySerAspIle 186
 Db 430 GTGAGTAGTGGTGGAGTGATCTGGTGGAGTGGATCTGGTGGAGCGGAAGTGATATT 489
 Qy 187 GluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSer 206
 Db 490 GTTATGACACAACTCACCTGCAAGTCTTGTGTTAGCCCTTGACAAAGCAAGCACTAAGT 549
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 ACCESSION AF003707
 VERSION AF003707.1 GI:3322218
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM
 REFERENCE 1 (bases 1 to 687)
 AUTHORS Amerdorfer,P., Wong,C., Chen,S., Smith,T., Deshpande,S.,
 Sheridan,R., Finnern,R. and Marks,J.D.
 TITLE Molecular characterization of murine humoral immune response to
 botulinum neurotoxin type A binding domain as assessed by using
 phage antibody libraries
 JOURNAL Infect. Immun. 65 (9), 3743-3752 (1997)
 MEDLINE 97427959
 PUBMED 9284147
 REFERENCE 2 (bases 1 to 687)
 AUTHORS Amerdorfer,P.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAY-1997) Anesthesia, University of California at San
 Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 REFERENCE 3 (bases 1 to 687)
 AUTHORS Amerdorfer,P.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-1998) Anesthesia, University of California at San
 Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 REMARK Sequence update by submitter
 COMMENT On Jul 16, 1998 this sequence version replaced gi:2306928.
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 /clone="1C9"
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 /db_xref="GI:3322218"
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 CDS
 Alignment Scores:
 Pred. No.: 2e-65 Length: 687
 Score: 1009.00 Matches: 195
 Percent Similarity: 84.74% Conservative: 16
 Best Local Similarity: 78.31% Mismatches: 18
 Query Match: 58.49% Indels: 20
 DB: 12 Gaps: 2
 US-10-089-278-6 (1-329) x AF003707 (1-687)
 Qy 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
 Db 1 CAGTGCAGCTGAAGCAGTCAGGGGCTGAGCTGGTGGGCTGGGGTCTCAGTGAAGATT 60

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Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 61 TCTGCAAGGTTCTGGCTACACATTCATCATGATATGCTGTGCACCTGGGTGAAGCAGAGT 120
Qy 88 HisAlaLysSerLeuGluTrpLleGlyLeuLysSerThrTyrTyrGlyAspProSerTyr 107
Db 121 CATGCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTACTATGTTGATGCTGACTAC 180
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 181 AACCCGAAGTTCAAGGCAAGGCACATTCAGTGTAAACAAGTCCCTCCAAACACAGCCTAT 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaAaGSerAsp 147
Db 241 ATGGAACCTCCAGACTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGGGGT 300
Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
Db 301 AAGGGT-----GCTATGCACTATTGGGCTCAAGGAACCTCAGTCACCGTCC 345
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlySerAspLleGlu 187
Db 346 TCC-----TCAGACATCGAG 360
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrLysSerCys 207
Db 361 CTACTCAGTCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGGCCCATCATATCTCTGC 420
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLys 227
Db 421 AGAGCCAGTGAAGTGTGTATGATGTAATAGTTTATGCACTGGTATACCAGCAGAAA 480
Qy 228 ProGlyGlnProProLysLeuLeuLleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db 481 CCAGGACAGCCACCCAACTCCCTCATCTATCGTATCCCAACTAGAAATCTGGGATCCCT 540
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrLleAspProValGlu 267
Db 541 GCCAGGTTTCACTGGCAGTGGTCTAGGACAGACTTCACCCCTCACCATTAACTCTGTGGAG 600
Qy 268 GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 601 GCTGATGATGTGCAACTATTACTGTGAGCAAGTAATGAGGATCGGTACAGCTTCGGA 660
Qy 288 GlyGlyThrLysLeuGluLleLysArg 296
Db 661 GGGGGGACCAAGCTGGAAATAAAACGG 687

RESULT 9
AX111698 LOCUS AX111698 906 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0125415.
ACCESSION AX111698
VERSION AX111698.1 GI:13927963
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1. Cichutek,K. and Engelstaedter,M.
AUTHORS Gene transfer in human lymphocytes using retroviral scfv cell
TITLE targeting
JOURNAL Patent: WO 0125415-A 5 12-APR-2001;
Bundesrepublik Deutschland LET (DE)
FEATURES
location/Qualifiers
source 1..906
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="scfv kodierende Sequenz"
ORIGIN
Alignment Scores:
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Pred. No.: 6,46e-65 Length: 906
Score: 1004.00 Matches: 196
Percent Similarity: 78.90% Conservative: 47
Best Local Similarity: 63.64% Mismatches: 51
Query Match: 58.20% Indels: 14
DB: Gaps: 4

US-10-089-278-6 (1-329) x AX111698 (1-906)
Qy 1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysIle 20
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Qy 21 LeuLleLeuLeuValAlaTrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40
Db 61 CTAAATCTCTGTGTGGCTTGGTGGGGTTTGGACCACTGCCGAAGTTTCGACTGCCCGA 120
Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
Db 121 CGGGCCAGCCGCCCATGGCCAGGTACAGCTGCAGAGTCAGGAGCAGCAAAATGAAAAG 180
Qy 61 ProGlyValSerValLysLysSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 181 CCGGGGAGTCTCTGAAATCTCCTGTAAGGGTTTGGATACGACTTTAGCACCTACTGG 240
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpLleGlyLeuLysSerThr 100
Db 241 ATCGCTGGTGGCCAGATGCCCGGGAAGGCTCGAGTACATGGGCTCATCTATCCT 300
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 301 GGTGACTCTGACACCAATAACACCCGCTCTTCCAAAGGCCAGGTACCACATCTCAGCCGAC 360
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 361 AAGTCCATCAGCACCCCTCCTGTCAGTGGAGCAGCCTGAAGCCTCGGACCCGCAATG 420
Qy 141 TyrTyrCysAlaArgSerAspGly-----AsnTyrGlyTyr 152
Db 421 TATTACTGTGGAGAGTCTCTGGATATTGTAGTAGTACCAGCTGTCTATGACTAC---TAC 477
Qy 153 TyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrValSerSerGlyGlyGly 172
Db 478 TACTACTACATGACGCTCTGGGCGCGGGAACCTGCTCACCCTCTCGAGAGGTGGAGGC 537
Qy 173 GlySerGlyGlyGlySerGlyGlyGlySerAspLleGluLeuThrGlnSerPro 192
Db 538 GGTTCAGGGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGTGTATGATGCCAGTCTCCT 597
Qy 193 SerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSer 212
Db 598 TCCACCTGTCTGCATCTCTAGGACAGACAGTCCACCATGACTTCCGGGCGCAGTCAGAAC 657
Qy 213 ValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLysProGlyGlnProPro 232
Db 658 ATTAATATCTGG-----TTGGCCTGTATCAGCAGAAACCAGGAAAGCCCT 705
Qy 233 LysLeuLeuLleTyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGly 252
Db 706 AAGCTCTGTATCTATTAAGGGCTCCACTTCTCACCATCAGCGGCTCGAGCCTGATGATTTGCA 765
Qy 253 SerGlySerGluSerAspPheThrLeuThrIleAspProValGluGluAspAspAlaAla 272
Db 766 AGTGGATCTGGGACAGAAATTCCTCTCACCATCAGCGGCTCGAGCCTGATGATTTGCA 825
Qy 273 ValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGlyGlyThrLysLeu 292
Db 826 AGTTATTACTGT---CAACGGTATGATGACTGTGCTGTCGCGCAAGGACCAAGCTG 882
Qy 293 GluLysArgAlaAlaAlaSer 300
Db 883 GAGATCAACGTCGGCCGATCG 906
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[illegible]

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Qy	101	TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLeuGlnSerGlyAlaGluLeuValAsp	120	
Db	226	GGAAATGGAGATCACTAATACATGATGGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC	285	
Qy	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140	
Db	286	AAATCCTCAGACACAGCTACATGAGCTCAGCAGCGCTGACCTCTGTGACTCTGGCGTC	345	
Qy	141	TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly	160	
Db	346	TATTTCTGTGCA-----GATGGTAACGTA--TATTACTATGCTATGACTACTGGGT	396	
Qy	161	GlnGlyThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlyGlyGlyGly	180	
Db	397	CAAGSAACCTCAGTACCGCTCTCCTCAGGTGGAGCGGTTCAAGTGGCGCGCTCTGGC	456	
Qy	181	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly	200	
Db	457	GGTGGCGGATCGCAATTTGTTCTACCCAGTCTCTGCTTCTTATCTGTATCTCTGGG	516	
Qy	201	GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe	220	
Db	517	CAGAGGGCCACCATCTCATGCGGGCCAGCAAAAGTGTCACTATCTGCTATAGTTAT	576	
Qy	221	MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer	240	
Db	577	ATGCATCTGGTACCACAGAAACAGACAGCCACCCAACTCTCATCTATCTTGTGATCC	636	
Qy	241	AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGlySerGlySerPhe	260	
Db	637	AACTAGATCTGGGTCTCCCTGCGAGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACC	696	
Qy	261	LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet	280	
Db	697	CTCAACATCCATCTCTGTGGAGGAGGATGTGCAACCTATTACTGTGACACAGTAGG	756	
Qy	281	GluAspProTyrThrPheGlyGlyThrLysLeuGluLeuIleLysArgAlaAla	299	
Db	757	GAGCTTCTCGGAGCTTCGGTGGAGGACCAAGCTGGAATCAACGGGGCGGCCA	813	
RESULT 13				
AX100194				
LOCUS	AX100194	876 bp	DNA	linear
DEFINITION	Sequence 101 from Patent WO0119992.			
ACCESSION	AX100194			
VERSION	AX100194.1	GI:13539109		
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	1			
AUTHORS	Scheifflinger, F., Kerschbaumer, R., Falkner, F.G. and Dörner, F.			
TITLE	Factor ix/factor ixa antibodies and antibody derivatives			
JOURNAL	Patent: WO 0119992-A 101 22-MAR-2001;			
	Baxter Aktiengesellschaft (AT)			
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	/db_xref="taxon:32630"			
	/note="scFv region"			
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Alignment Scores:				
Pred. No.:	4.34e-64	Length:	876	
Score:	992.50	Matches:	195	
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Query Match:	75.54%	Indels:	3	
DB:	6	Gaps:	2	

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LOCUS	Synthetic construct clone 1B6 anti BoNT/A Hc scFv antibody gene,				
DEFINITION	partial cds.				
ACCESSION	AF003705				
VERSION	AF003705.1	GI:3322214			

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Db      301  AAGGGT-----GCTATGAGTACTTGGGGTCAAGGCACCGTCCCGTC 345
Qy      168  SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerAspIleGlu 187
Db      346  TCC-----TCAGACATCGAG 360
Qy      188  LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db      361  CTCACCTCAGCTCCAGCTCTTTGGCTGTGTCTCTAGGGCAGAGGCCCATCATATCCTGC 420
Qy      208  ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLys 227
Db      421  AGAGCCAGTGAAGTGTGATAGTATGCAATAGTATTTATGCACCTGGTACCAGCGAGAAA 480
Qy      228  ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db      481  CCAGGACAGCCACCCAACTCCTCATCTATCGTGATCCAACTAGAACTTGGATCCCT 540
Qy      248  AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db      541  GCCAGGTTTCAGTGGCAGTGGTCTAGGACAGACTTCACCCCTCACCATTAACTCTGTGGAG 600
Qy      268  GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db      601  GCTGATGATGTTGCAACCTATTACTGTACGAAAGTAATGAGGATCCTCCCAGTTCGGT 660
Qy      288  GlyGlyThrLysLeuGluIleLysArg 296
Db      661  GCTGGGACCAAGCTGGAGCTGAACCC 687

RESULT 15
CQ881538
LOCUS      897 bp      DNA      linear      PAT 11-OCT-2004
DEFINITION      Sequence 44 from Patent WO2004083373.
ACCESSION      CQ881538
VERSION      CQ881538.1 GI:54034468
KEYWORDS
SOURCE      Mus sp.
ORGANISM      Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
AUTHORS      Toms, G., Routledge, E. and Mekseepalard, C.
TITLE      Antibody against the g glycoprotein of respiratory syncytial virus
JOURNAL      Patent: WO 2004083373-A 44 30-SEP-2004;
THE UNIVERSITY OF NEWCASTLE UPON TYNE (GB)
FEATURES
source      1..897
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Pred. No.:      991.00      Matches:      191
Score:      83.85%      Conservative:      27
Percent Similarity:      73.46%      Mismatches:      40
Best Local Similarity:      57.45%      Indels:      2
Query Match:      6
DB:      2

US-10-089-278-6 (1-329) x CQ881538 (1-897)

Qy      41  AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
Db      46  GCGGCCAGCGCGCCATGGCCAGGTGCAGCTGCAGCAGTCAGGGCCTGAGGTGGTGAGG 105
Qy      61  ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
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Search completed: August 23, 2005, 15:48:23
Job time : 3953 secs

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Qy      81  MetSerTyrValLysGlnSerHisAlaLysSerLeuGluTyrIleGlyLeuIleSerThr 100
Db      166  ATGCACCTGGGTGAAGCAGAGTCACGCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACT 225
Qy      101  TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db      226  TACTATGTGTAAATCCAAATTACAAACAGAAAGTTTAAGGGCAAGGCCACCAATGCTGTAGAC 285
Qy      121  LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db      286  AAATCCTCCAGCAGCCCTATATGGAACCTGCGACATATGACATATGAGGATTTCTGCCATC 345
Qy      141  TyrTyrCysAlaArgSerAspGly---AsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyr 159
Db      346  TATTACTGTGCAAGATCGGATATGATTACGGCGCGGGGGGTATGCTATGACTACTGG 405
Qy      160  GlyGlnGlyThrThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySer 179
Db      406  GGCCAAAGGACACACGCTCACCGTCTCGAGTGTGGAGCGGTTTCAGGGCGAGGTGGCTCT 465
Qy      180  GlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeu 199
Db      466  GCGGTAGTGTGCACAGGATGTTTGTATGATGACCCAGACTCTCTCTCCCTGCTGTGACTTT 525
Qy      200  GlyGlnArgAlaThrIleSerCysArgAlaSerGluSer---ValAspSerTyrGlyAsp 218
Db      526  GGAGATCAAGCTCCATCTCTTGCAGATCTAGTCAGAACATTGTACATAGTATGGAAC 585
Qy      219  SerPheMetHisTyrTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArg 238
Db      586  ACCTATTTAGAGTGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAA 645
Qy      239  AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
Db      646  GTTTCACACCGAATTTCTGGGGTCCAGACAGAGTTCAGTGGCAGTGGATCAGGGACAGAT 705
Qy      259  PheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGln 278
Db      706  TTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAA 765
Qy      279  SerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 298
Db      766  GGTTCACATATTCCTGGGACGTTCCGTGGAGGGACCAAGCTGGAGATCTCCCGCGCCGCA 825
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 12:01:37 ; Search time 536 Seconds

(without alignments)
3633.573 Million cell updates/sec

Title:

US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNLRAGKVDQASKI.....GSGGGGGGGGSGGASPVQFI 329

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2.1/USPTO.spool.p/US10089278/runat.23082005.121733.29323/app_query.fasta.1.519

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi

-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 16Dec04.*

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3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1725	100.0	1030	5 AAF61509	Aaf61509 DNA encod
2	1239	71.8	990	5 AAF61511	Aaf61511 DNA encod
3	1202.5	69.7	946	5 AAF61512	Aaf61512 DNA encod
4	1186.5	68.8	927	5 AAF61510	Aaf61510 DNA encod
5	1094	63.4	868	10 ACC57513	Acc57513 Newcastle

6	1009.5	58.5	744	10	ADL07528	Adl07528 P. pastor
7	1004	58.2	806	5	AAf61513	Aaf61513 DNA encod
8	994	57.6	1094	3	AAa60982	Aaa60982 Antibody
9	993.5	57.6	2190	4	AAf30729	Aaf30729 Antibody
10	992.5	57.5	876	4	AAf30734	Aaf30734 DNA encod
11	992.5	57.5	969	4	AAf30730	Aaf30730 Antibody
12	991	57.4	897	13	ADs88776	Ads88776 Nucleotid
13	991	57.4	1698	3	AAz43431	Aaz43431 Fv-antibo
14	983	57.0	925	3	AAz44206	Aaz44206 Murine de
15	983	57.0	925	3	AAz58664	Aaz58664 Antibody
16	980	56.8	1010	4	AAf73076	Aaf73076 Anti-digo
17	978	56.7	780	2	AAx06088	Aax06088 Anti-digo
18	978	56.7	780	2	AAv81140	Aav81140 Anti-digo
19	978	56.7	780	2	AAv81140	Aav81140 Anti-digo
20	974.5	56.5	1817	8	ACC79607	Acc79607 Plasmid p
21	948.5	55.0	1906	10	ADD13791	Add13791 Plasmid p
22	947.5	54.9	756	4	AAf11887	Aaf11887 cDNA enco
23	946.5	54.9	891	2	AAf36907	Aaf36907 FvKC-II-K
24	935.5	54.2	717	4	AAc85539	Aac85539 scFv 508F
25	935.5	54.2	717	10	AAf51099	Aaf51099 Human neu
26	935.5	54.2	717	12	ADJ88112	Adj88112 Human bec
27	935	54.2	996	2	AAT36906	At36906 FvKC-II g
28	927	53.7	786	13	ADT91212	Adt91212 Single ch
29	924	53.6	993	9	AAf56799	Aaf56799 Chemokine
30	924	53.6	2199	4	AAf30727	Aaf30727 Anti-FIX/
31	923.5	53.5	1734	4	AAa89072	Aaa89072 Activatin
32	923	53.5	876	2	AAV10390	Aav10390 Monoclonal
33	923	53.5	888	4	AAf30732	Aaf30732 DNA encod
34	922.5	53.5	2214	13	ADR43336	Adr43336 Anti-NGK2
35	920	53.3	1668	4	AAa89071	Aaa89071 Activatin
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37	920	53.3	1725	2	AAx01651	Aax01651 Bispecific
38	919	53.3	978	4	AAf30728	Aaf30728 Anti-FIX/
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40	918	53.2	2952	6	ABK13464	Abk13464 DNA encod
41	917.5	53.2	1605	4	AAh78156	Aah78156 Nucleotid
42	917.5	53.2	1605	6	ABA04532	Abao4532 Murine MA
43	917.5	53.2	1605	6	ABX00129	Abx00129 Mouse DNA
44	917.5	53.2	1605	6	ABK71335	Abk71335 DNA encod
45	916.5	53.1	797	2	AAT36908	At36908 Yeast-FvK

ALIGNMENTS

RESULT 1
AAF61509
ID AAF61509 standard; DNA; 1030 BP.

XX AAF61509;

XX 11-SEP-2003 (revised)

DT 25-JUN-2001 (first entry)

XX DNA encoding SNV-env leader/human 7A5-scFv fusion construct.

DE T lymphocyte; antibody; single chain variable antibody; scFv; human;

KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;

KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;

KW acquired immune deficiency syndrome; severe combined immune deficiency;

KW T cell lymphoma; fusion construct; ds.

XX Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX Key

FT Location/Qualifiers

FT 44..178

FT /tag= a

FT /product= "SNV-env leader peptide"

FT /note= "No stop codon given"

FT 179..1030

FT /tag= b

FT /product= "7A5-scFv"

FT /note= "no stop codon given"
 TT /partial
 PN DE19946142-A1.
 XX
 XX 29-MAR-2001.
 XX
 XX 27-SEP-1999; 99DE-01046142.
 XX
 XX 27-SEP-1999; 99DE-01046142.
 PR (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
 XX
 XX Cichutek K, Engelstaedt M;
 XX WPI; 2001-246140/26.
 DR P-PSDB; AAB70840.
 XX
 XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
 PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
 PT variable antibody fragment.
 XX
 PS Claim 1; Fig 1; 18pp; German.
 XX
 XX This invention describes a novel cell-targeting vector (A) containing a
 CC DNA sequence (i) encoding a single-chain variable antibody fragment
 CC (scFv). The products of the invention have antiviral, cytostatic and
 CC immunostimulant activity and can be used in gene therapy, immunization
 CC and diagnosis particularly of T cell-associated diseases, specifically
 CC acquired immune deficiency syndrome (AIDS), severe combined immune
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 CC human B cells, and 1000 fold selectivity over other human cells. A vector
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
 CC fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 CC determine transformation. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
 CC showing the high selectivity for human T cells. This sequence encodes the
 CC SNV-env leader/human 7A5-scFv fusion construct used in the construction
 CC of novel cell targeting vectors described in the invention. (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 1030 BP; 232 A; 244 C; 304 G; 250 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.57e-103 Length: 1030
 Score: 1725.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-089-278-6 (1-329) x AAF61509 (1-1030)

QY 1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyValAspGlnAlaSerLysile 20
 DB 44 ATGGACTGTCTACCAACCTCCAGTCCGCTGAGGGTAAGTTGACAGGGCAGCAAAATC 103
 QY 21 LeuIleLeuLeuValAlaTrpTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40
 DB 104 CTAATTCCTCTGGCTTGGTGGGGTTGGGACCACCTCCCAAGTTTCAGCTGCCCGA 163
 QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
 DB 164 GCGGCCCGCCGCGCATGGCCGAGGTCAAGCTGCAGCAGTCAGGGGGCTGAGCTGGTGG 223
 QY 61 ProGlyValSerValLysileSerCysLysGlySerGlyThrThrPheThrAspTyrGly 80
 DB 224 CTTGGGGTCTCAGTGAAGATTTCTGCAAGGGTTCTGGCTACACATTCAGTGAATGGT 283

QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
 DB 284 ATGAGCTGGTCAAAACAGAGTCAATGCAAGAGTCTAGAGTGGATTGGACTTATTAGTACT 343
 QY 101 TyrTyrGlyAspProSerTrpAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
 DB 344 TACTATGGTGTAGTCTAGTTACAAACAGAGGTTCAAGGGCAAGGCCCAATAGCTGTAGAC 403
 QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
 DB 404 AAATCTCTCAACACAGAGCTATTITGGAACTTGGCACTGACATCTGAGGATTTGCGCAT 463
 QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
 DB 464 TATTAATTGTGCAAGATCGGATGTAATTACGGGTATTACTATGCTTTGGACTACTGGGGC 523
 QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlySerGlyGlySerGly 180
 DB 524 CAAGGCACCTACCGTCAACCGTCTCTCAGGTGAGCGGTTCAAGGGCAGGTGGCTCTGGC 583
 QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
 DB 584 GGTGGCGGATCGGATATCGAGCTCACTCAGTCTCCATCTCTTTGGCTGTCTCTAGGG 643
 QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
 DB 644 CAGAGGGCCACCATATCTCTGAGAGCCAGTGAAGTGTGTATAGTTATGGCGATAGTTT 703
 QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
 DB 704 ATGCACCTGGTATCAGCAGAAACAGGACAGCCCAAACTCTCATCTATCTGTCGATCC 763
 QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
 DB 764 AACCTAGATTCGGAGTCCCTGCCAGTTCAGTGGCAGTGGTCTGAGTCAGACTTCACT 823
 QY 261 LeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
 DB 824 CTCACCATCGATCTCTGGAGGAAGATGATGCTGCAGTGTATTACTGTCTGCAAAAGTATG 883
 QY 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaSer 300
 DB 884 GAAGATCCGTACACGTTCCGAGGGGGGCAAGAGTGGAAATAAACCGGGCGCCGATCG 943
 QY 301 GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 320
 DB 944 GGCTCCGGGGGGGTGGTTCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1003
 QY 321 SerGlyAlaSerProValGlnPheIle 329
 DB 1004 TCTGGCGCCAGGCCAGTCCAGTTTATC 1030
 RESULT 2
 AAF61511
 ID AAF61511 standard; DNA; 990 BP.
 XX
 AC AAF61511;
 XX
 DT 11-SEP-2003 (revised)
 DT 25-JUN-2001 (first entry)
 XX
 DE DNA encoding SNV-env leader/human 7B2-scFv fusion construct.
 XX
 KW T lymphocyte; antibody; single chain variable antibody; scFv; human;
 KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
 KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
 KW acquired immune deficiency syndrome; severe combined immune deficiency;
 XX T cell lymphoma; fusion construct; ds.
 OS Homo sapiens.
 OS Spleen necrosis virus.
 OS Chimeric.
 XX

FH Key Location/Qualifiers
 FT 1..135
 FT /*tag= a
 FT /product= "SNV-env leader peptide"
 FT /note= "No stop codon given"
 CDS 136..990
 FT /*tag= b
 FT /product= "7B2-scFv"
 FT /note= "no stop codon given"
 FT /partial
 XX DE19946142-A1.
 XX
 XX 29-MAR-2001.
 XX
 XX 27-SEP-1999; 99DB-01046142.
 XX
 XX 27-SEP-1999; 99DE-01046142.
 XX
 XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.
 XX
 XX Cichutek K, Engelstaedter M;
 PI
 XX WPI; 2001-246140/26.
 DR P-PSDB; AAB70842.
 XX
 XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
 PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
 FT variable antibody fragment.
 PT
 XX Claim 1; Fig 3; 18pp; German.
 PS
 XX This invention describes a novel cell-targeting vector (A) containing a
 CC DNA sequence (1) encoding a single-chain variable antibody fragment
 CC (scFv). The products of the invention have antiviral, cytostatic and
 CC immunostimulant activity and can be used in gene therapy, immunization
 CC and diagnosis particularly of T cell-associated diseases, specifically
 CC acquired immune deficiency syndrome (AIDS), severe combined immune
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 CC human B cells, and 100 fold selectivity over other human cells. A vector
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
 CC fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 CC determine transfection. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa.
 CC showing the high selectivity for human T cells. This sequence encodes the
 CC SNV-env leader/human 7B2-scFv fusion construct used in the construction
 CC of novel cell targeting vectors described in the invention. (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 990 BP; 210 A; 263 C; 289 G; 228 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.: 5.84e-72 Length: 990
 Score: 1239.00 Matches: 243
 Percent Similarity: 82.23% Conservative: 30
 Best Local Similarity: 73.19% Mismatches: 45
 Query Match: 71.83% Indels: 14
 DB: 5 Gaps: 5

 US-10-089-278-6 (1-329) x AAF61511 (1-990)

 QY 1 MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysile 20
 DB 1 ATGGACTGTCTACCAACCTCCGATCCGCTGAGGGTAAAGTTGACCGAGCGCAAAATC 60

 QY 21 LeuileLeuLeuValAlaTrpPheGlyThrAlaGluValSerThrAlaArg 40
 DB 61 CTAAATCTCTTGTGGCTTGGTGGGGTGGGACCACTGCCGAAGTTTCGACTGCGCGA 120

QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
 DB 121 GCGGCCAGCCGCCCATGGCCAGGTGCAGCTCGAGCTGGAACAA 180

 QY 61 ProGlyValSerValLysileSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
 DB 181 CTTGGGGCCTCAGTGAGGATGCTCTGCNAGGCTTCTGGCTACGCCTTTACTACTACTGG 240

 QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuile----- 98
 DB 241 ATGCACTGGGTAACACAGAGCGCTGGACAGGGTCTGGAATGGATTGGATACATTAACTCT 300

 QY 99 SerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThr 118
 DB 301 ACCACTGATTATTAATCTGAC-----TACAATCTCAAGTTCAAGGACCAAGGCCACATTGACT 354

 QY 119 ValAspLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSer 138
 DB 355 GCAGACAAATCTCCAGTACAGCTACATGCACTGAGCAGCCTGACATCTGAGGACTCT 414

 QY 139 AlaIleTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyr 158
 DB 415 GCAGTCTATTACTGTCAAGATCG-----GGTGGTCTCTATGCTATGGACTAC 462

 QY 159 TrpGlyGlnGlyThrThrValSerSerGlyGlyGlyGlyGlySerGlyGlyGly 178
 DB 463 TGGGGGCAAGGGACCACTGCTCCTCAGGTGGAGCGGTTCAGCGGAGGTGGC 522

 QY 179 SerGlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSer 198
 DB 523 TCTGGGGTGGCGGATCGGACATCGAGCTCAGTCTCCAGCAATCATGCTGCACT 582

 QY 199 LeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAsp 218
 DB 583 CCAGGGGAGAGGTGCACTAATCCTGCAGTGCAGCTCAAGTGA----- 627

 QY 219 SerPheMetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArg 238
 DB 628 AGTTATCATGCATCTGGTTCCAGCAGAGCCAGGCACCTTCTCCCAAACTCTGGATTATAGC 687

 QY 239 AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
 DB 688 ACATCCAACTGGCTTCTGGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 747

 QY 259 PheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGln 278
 DB 748 TACTCTCTCACAATCAGCCCAATGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCA 807

 QY 279 SerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 298
 DB 808 AGGAGTAGTTATCCCATTCAGTTCCGCTCGGGCACCAGCTGGAAATCAAAACGGCGGCC 867

 QY 299 AlaSerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlyGlySerGly 317
 DB 868 GCATCGGGCTCCGGGGCGGTGTTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 927

 QY 318 GlyGlyGlySerGlyAlaSerProValGlnPheile 329
 DB 928 GGT 963

 RESULT 3
 AAF61512
 ID AAF61512 standard; DNA; 946 BP.
 XX
 AC AAF61512;
 XX
 XX 11-SEP-2003 (revised)
 DT 25-JUN-2001 (first entry)
 XX
 DE DNA encoding SNV-env leader/human 7E4-scFv fusion construct.
 XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
 KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
 KW

KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
 KW acquired immune deficiency syndrome; severe combined immune deficiency;
 KW T cell lymphoma; fusion construct; ds.
 XX

OS Homo sapiens.
 OS Spleen necrosis virus.
 OS Chimeric.

Key Location/Qualifiers
 CDS 1..135
 FT /tag= a
 FT /product= "SNV-env leader peptide"
 FT /note= "No stop codon given"
 FT 136..946
 CDS
 FT /tag= b
 FT /product= "7E4-scfv"
 FT /note= "no stop codon given"
 FT /partial
 XX

PN DE19946142-A1.
 XX
 XX 29-MAR-2001.
 XX 27-SEP-1999; 99DE-01046142.
 XX 27-SEP-1999; 99DE-01046142.
 XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.

XX Cichutek K, Engelstaedter M;
 XX WPI; 2001-246140/26.
 DR P-PSDB; AAB70843.
 XX
 XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
 PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
 PT variable antibody fragment.
 XX
 XX Claim 1; Fig 4; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a
 CC DNA sequence (1) encoding a single-chain variable antibody fragment
 CC (scfv). The products of the invention have antiviral, cytostatic and
 CC immunostimulant activity and can be used in gene therapy, immunization
 CC and diagnosis particularly of T cell-associated diseases, specifically
 CC acquired immune deficiency syndrome (AIDS), severe combined immune
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 CC human B cells, and 1000 fold selectivity over other human cells. A vector
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
 CC fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 CC determine transfection. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa.
 CC showing the high selectivity for human T cells. This sequence encodes the
 CC SNV-env leader/human 7E4-scfv fusion construct used in the construction
 CC of novel cell targeting vectors described in the invention. (Updated on
 CC 11-SEP-2003 to standardise OS field)

SQ Sequence 946 BP; 199 A; 249 C; 276 G; 222 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.32e-69 Length: 946
 Score: 1202.50 Matches: 236
 Percent Similarity: 83.12% Conservative: 30
 Best Local Similarity: 73.75% Mismatches: 47
 Query Match: 69.71% Indels: 7
 DB: 5 Gaps: 4

US-10-089-278-6 (1-329) x AAF61512 (1-946)

QY	1	MetAspCysLeuThrAsnLeuArgSerAlaGluGlyLysValAspGlnAlaSerLysIle	20
DB	1	ATGGACTGCTCACCACCTCCGATCCGCTGAGGGTAAAGTTGACCAAGCGAGCAAAATC	60
QY	21	LeuIleLeuValAlaLalTrpGlyPheGlyThrAlaGluValSerThrAlaArg	40
DB	61	CTAATTCTCTTGTGGTGGGGTGGGACCACTCCGCAAGTTTCGACTGCGCGA	120
QY	41	AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyValAlaGluLeuValArg	60
DB	121	GGGGCCCGCCAGCCGATGGCCGAGGTCAAGCTGCAGCAGTCAGGGGCTGAGCTGGTGG	180
QY	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly	80
DB	181	CTGGAGCTTCAGTGAAGCTGCTCTGCAAGACTTCTGGCTTCTCTTCCACCACTACTG	240
QY	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuLeuSerThr	100
DB	241	ATGAAGCTGGTGAAGCTGAGGCTGGACAAGCCCTTGAAGTGGATTTGGCATGATTCTCT	300
QY	101	TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp	120
DB	301	TCCGATAGTGAACCTAGTTTAACTCAGAGGTTCAAGGACAAGCCACACTGACTGTAGAC	360
QY	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140
DB	361	AAATCTCCAGCACAGCCTACATGCAACTCAGCAGCCGACATCTGAGGACTCTCGCGTC	420
QY	141	TyrTyrCysAlaArgSer---AspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrp	159
DB	421	TATTACTGTCAAGATCTCTTTATGCTAACTACCCCTCCTGGTTACT-----TACTGG	474
QY	160	GlyGlnGlyThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySer	179
DB	475	GGCCAAGGACCACCGCTCACCCTCCTCAGGTGGAGCGGTTTCAGCCGAGGTGGCTCT	534
QY	180	GlyGlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeu	199
DB	535	GGCGGTGGCGGATCGACATCGAGCTCACTCAGTCTCCACCAACCACCATGCTCTCCC	594
QY	200	GlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSer	219
DB	595	GGGGAGAGATCACTATCACTGCAGTGCAGCTCAAGTATATAAGTTTC-----AAT	645
QY	220	PheMetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAla	239
DB	646	TACTTCATTTGGTATCAGCAGAACCCAGGATTCCTCCCTAAACTCTTGATTATAGACA	705
QY	240	SerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPhe	259
DB	706	TCCAATCTGGCTTCCTGGAGTCCCGCTCCTCAGTGGCAGTGGGTCTGGGACCTCTTAC	765
QY	260	ThrLeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSer	279
DB	766	TCTCTCACAATTGGCCACCATGGAGGTGAAGATTTGGCCACTTACTTCTGCCAGCGGT	825
QY	280	MetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla	299
DB	826	AGTAGTATACCGTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGCGGGCGCGCA	885
QY	300	SerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlyGlySerGlyGly	318
DB	886	TCGGGCTCCGGGGCGGTCTCTGTGGTGGTGGTCTTGGTGGTGGTGGTGGTGGTGGT	945
	RESULT 4		
	AAF61510		
ID	AAF61510	standard; DNA; 927 BP.	
XX	XX		
AC	AAF61510;		
XX	XX		
DT	11-SEP-2003	(revised)	
DT	25-JUN-2001	(first entry)	
XX	XX		

DNA encoding SNV-env leader/human K6-scFv fusion construct.

DE T lymphocyte; antibody; single chain variable antibody; scFv; human;
XX cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KW acquired immune deficiency syndrome; severe combined immune deficiency;
KW T cell lymphoma; fusion construct; ds.

OS Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.

XX

XX Key Location/Qualifiers

XX CDS 1..135

XX /*tag= a

XX /product= "SNV-env leader peptide"

XX /note= "No stop codon given"

XX CDS 136..927

XX /*tag= b

XX /product= "K6-scFv"

XX /note= "no stop codon given"

XX /partial

XX DE19946142-Al.

XX 29-MAR-2001.

XX 27-SEP-1999; 99DE-01046142.

XX 27-SEP-1999; 99DE-01046142.

XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.

XX Cichutek K, Engelstaedter M;

XX WPI; 2001-246140/26.

XX P-PSDB; AAB70841.

XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT variable antibody fragment.

XX Claim 1; Fig 2; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (I) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transformation. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa.
CC showing the high selectivity for human T cells. This sequence encodes the
CC SNV-env leader/human K6-scFv fusion construct used in the construction of
CC novel cell targeting vectors described in the invention. (Updated on 11-
CC SEP-2003 to standardise OS field)

XX SQ Sequence 927 BP; 205 A; 238 C; 277 G; 207 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.41e-68 Length: 927
Score: 1186.50 Matches: 229
Percent Similarity: 79.69% Conservative: 26
Best Local Similarity: 71.56% Mismatches: 54
Query Match: 68.78% Indels: 11

DB:	5	Gaps:	2
US-10-089-278-6 (1-329) x AAF61510 (1-927)			
Qy	1 MetAspCysLeuThrAsnLeuAArgSerAlaGluGlyValAspGlnAlaSerLysLeu 20		
Db	1 ATGGACTGTCTCACCAACCTCCGATCCGCTGAGGGTAAAGTTGACCAAGCGGAGCAAAATC 60		
Qy	21 LeuLeuLeuValAlaThrTrrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40		
Db	61 CTAATTCTCCTTGTGGCTTGTGGGGTTTGGGACCACTGCCGAAGTTTGCACCTGCCGCGA 120		
Qy	41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60		
Db	121 GCGGCCAGCCGCCATGGCCGAGGTCAAGCTCAGAGGTGAGGACTGAACCTTGTGAAG 180		
Qy	61 ProGlyValSerValLysLysSerCysLysGlySerGlyThrThrPheThrAspTyrGly 80		
Db	181 CCTGGGGCTTCAGTGAATCTGTCTTGCAGGGCTTCTGGCTACACCTTCCACGACTACTGG 240		
Qy	81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpLysGlyLeuLeuSerThr 100		
Db	241 ATGCACCTGGTTGAAGCAGAGGCGCTTGGCAAGGCTTGGATCGGATCGGAGAGATTGATCCT 300		
Qy	101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120		
Db	301 GTTGATAGTTATATACTAACTCAAACTTCAAGGGCAAGCCACACTGACTGTAGAC 360		
Qy	121 LysSerSerAsnThrAlaTyrLeuLeuAlaArgLeuThrSerGluAspSerAlaIle 140		
Db	361 AAGTCTCCACACACAGCTACATGACCTCAGCAGGCTGACATCTGAGGACTCTCGCGTC 420		
Qy	141 TyrTyrCysAlaArgSerAspGlyAsnTyrTyrTyrTyrAlaLeuAspTyrTrpGly 160		
Db	421 TATTACTGTCAAGAAAGGGC-----TATGCTATGGACTACTGGGGC 462		
Qy	161 GlnGlyThrThrValSerSerGlyGlyGlySerGlyGlyGlyGlyGlySerGly 180		
Db	463 CAAGGACCAACGTACCTCCTCAGGTGGATGCGGTTCCAGCGGAGGTGGCTCTCGGC 522		
Qy	181 GlyGlyGlySerAspLeuLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200		
Db	523 GGTGGCGGATCGGACATCGAGCTCACTCAGTCACCAAGCAATCATGCTGTCCAGGG 582		
Qy	201 GlnArgAlaThrLysSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220		
Db	583 GAGAGGTCACCATGACCTGCGAGTGCAGCTCAAGTATA-----AGTTAC 627		
Qy	221 MetHisTrpTrpGlnGlnLysProGlyGlnProProLysLeuLeuLeuTyrArgAlaSer 240		
Db	628 ATGCACCTGGTACCAAGCAGAGCCAGGACCTCCCAAGAGATGGATTATGACACATCC 687		
Qy	241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260		
Db	688 AAATGGCTTCTGGAGTCCCTGCTGCTCAGTGGCAGTGGGTCTGGGACCTCTTATTCT 747		
Qy	261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280		
Db	748 CTCCCAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCATCAGCGGAGT 807		
Qy	281 GluAspProTyrThrPheGlyGlyThrLysLeuLeuLysArgAlaAlaAlaSer 300		
Db	808 AGTTACCCATGACGTTCTGGTGGAGGAGCAAGCTTGAATAAAGCGGCGGCGGATCG 867		
Qy	301 GlySerGlyGlyGlySerGlyGlySerGlyGlySerGlyGlyGlyGlyGlyGly 320		
Db	868 GGTCTCCGGGGCGGTGTTCTGGTGGTGGTCTGGTGGTGGTGGTGGTGGTGGTGGT 927		
RESULT 5			
ACC57513			
ID	ACC57513 standard; cDNA; 868 BP.		
XX			
AC	ACC57513;		

XX This invention describes a novel cell-targeting vector (A) containing a
 CC DNA sequence (1) encoding a single-chain variable antibody fragment
 CC (scFv). The products of the invention have antiviral, cytostatic and
 CC immunostimulant activity and can be used in gene therapy, immunization
 CC and diagnosis particularly of T cell-associated diseases, specifically
 CC acquired immune deficiency syndrome (AIDS), severe combined immune
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 CC human B cells, and 1000 fold selectivity over other human cells. A vector
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
 CC fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 CC determine transfection. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
 CC showing the high selectivity for human T cells. This sequence encodes the
 CC SNV-env leader/human 6C3-scFv fusion construct used in the construction
 CC of novel cell targeting vectors described in the invention. (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 906 BP; 204 A; 246 C; 262 G; 194 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,01e-56 Length: 906
 Score: 1004.00 Matches: 196
 Percent Similarity: 78.90% Conservative: 47
 Best Local Similarity: 63.64% Mismatches: 51
 Query Match: 58.20% Indels: 14
 DB: 5 Gaps: 4

US-10-089-278-6 (1-329) x AAF61513 (1-906)

QY 1 MetAspCysLeuThrAsnLeuArgSerAlaGluCysValAspGlnAlaSerLysile 20
 DB 1 ATGGACTGTCTCCACCACTCCGATCGCTAGGGTAAAGTTGACGAGCGGAGCAAAATC 60
 QY 21 LeuileuLeuValAlaTTPTrpGlyPheGlyThrThrAlaGluValSerThrAlaArg 40
 DB 61 CTAATTCCTCTGGGCTTGGTGGGGTATGGGACCACTGCCGAAGTTTCGACTGCCGA 120
 QY 41 AlaAlaGlnProAlaMetAlaGluValLysGlnGlnSerGlyAlaGluLeuValArg 60
 DB 121 CGGCCCCAGCGCCATGGCCAGGTACAGCTGCAGCAGTCAGGACGAGAAATGAAAAG 180
 QY 61 ProGlyValSerValLysileSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
 DB 181 CCCGGGAGTCTCTGAAAATCTCTGTAGGGTTTGGATACGACTTTAGCACCTACTGG 240
 QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
 DB 241 ATCGCTGGGTGGCCAGATGCCGGGAAAGGCTGGAGTACATGGGGCTCATCTATCCT 300
 QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
 DB 301 GGTGACTCTGACCAATATACAGCCCTCTTCAAGGCCAGGTCCACCATCTCAGCGGAC 360
 QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
 DB 361 AAGTCCATCAGCAGCGCTACCTGCAGTGGAGCAGCCTGAAGGCTCGGACACCGCCATG 420
 QY 141 TyrTyrCysAlaArgSerAspGly-----AnTyrGlyTyr 152
 DB 421 TATTACTGTGGAGAGTCTTGGATATTGTAGTAGTACCAGCTGCTATGACTAC---TAC 477
 QY 153 TyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrValThrValSerSerGlyGly 172
 DB 478 TACTACTACATGAGCTGTGGGCGCGGGAACCTGTCTACCGTCTCAGAGGTGGAGGC 537
 QY 173 GlySerGlyGlyGlySerGlyGlyGlySerAspIleGluLeuThrGlnSerPro 192
 DB 538 GGTTCAGGCGAGGTGCTCTGGCGGTGGGGATCGGACATCGTGATGACCCAGCTCCT 597

QY 193 SerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSer 212
 DB 598 TCACCTCTGTGCATCTGTAGAGACAGAGTCACCATGACTTGCAGGCGCCAGTCAGAAC 657
 QY 213 ValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLysProGlyGlnProPro 232
 DB 658 ATTAATATCTGG-----TTGGCTCGTATCAGCAGAAACCCAGGAAAGCCCT 705
 QY 233 LysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGly 252
 DB 706 AAGCTCTCTGATCTATAAGCGCTCCACTTTAGAGAGTGGGCTCCCGTCAAGGTTCAGCGC 765
 QY 253 SerGlySerGluSerAspPheThrLeuThrIleAspProValGluGluAspAlaAla 272
 DB 766 AGTGGATCTGGACAGAAATCTCTCACCATCAGCGGCTGCAGCTGATGATTTTGA 825
 QY 273 ValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeu 292
 DB 826 AGTTATTACTGT---CAACGGTATGATAGTACTGTGTCGTTCGGCCAGGACCAAGCTG 882
 QY 293 GluIleLysArgAlaAlaSer 300
 DB 883 GAGATCAAAACGTGGCGCGCATCG 906
 RESULT 8
 AAA60982
 ID AAA60982 standard; DNA; 1094 BP.
 XX
 AC AAA60982;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Antibody nucleotide sequence.
 XX
 KW Lida-protein; LDP; Lida-chromophore; LDC; antibody; lidamycin;
 KW antibiotic; anticancer; tumour; cancer; ds.
 XX
 OS Synthetic.
 XX
 FN CN1251840-A.
 XX
 PD 03-MAY-2000.
 XX
 PF 13-OCT-1999; 99CN-00121668.
 XX
 PR 13-OCT-1999; 99CN-00121668.
 XX
 PA (MEDI-) INST MEDICINAL BIOTECHNOLOGY CHINESE ACA.
 XX
 PI Zhen Y, Li S, Jiang M;
 XX
 DR WPI; 2000-432052/38.
 XX
 PT Constitutive fusion protein of ridamycin as anticancer antibiotic and
 PT single-chain antibody.
 XX
 PS Disclosure; Page 2-3; 18pp; Chinese.
 XX
 CC The present invention describes a fusion protein, designated Lidamycin,
 CC composed of Lida-protein (LDP) and Lida-chromophore (LDC), which acts as
 CC an anticancer antibiotic and single-chain antibody. LDP and LDC are
 CC joined via non-covalent bonds and can be splitted and recombined. A
 CC single-chain antibody scFv can specifically join with IV-type collagenase
 CC and can suppress its activity and in order to increase the permeability
 CC of medicine to capillary tubes and the penetrability to real tumour, DNA
 CC recombination and molecular recombination are used to prepare new-type
 CC constitutive fusion protein LDM-Fv of anticancer targeting medicine
 CC Lidamycin and single-chain antibody. Its molecular weight is about 37kDa.
 CC It has the activity to inhibit IV-type collagenase and strong intrusion-
 CC resistance kill action to cancer cells. It may be an ideal clinic
 CC medicine. The present sequence represents an antibody nucleotide sequence
 CC given in the exemplification of the present invention

XX Sequence 1094 BP; 230 A; 312 C; 325 G; 227 T; 0 U; 0 Other;
SQ

Alignment Scores:

Pred. NO.: 5.39e-56 Length: 1094
Score: 994.00 Matches: 197
Percent Similarity: 76.11% Conservative: 26
Best Local Similarity: 67.24% Mismatches: 46
Query Match: 57.62% Indels: 24
DB: 3 Gaps: 3

US-10-089-278-6 (1-329) x AAA60982 (1-1094)

```
Qy 46 MetAlaGluValLysLeuGlnSerGlyAlaGluValArgProGlyValSerVal 65
Db 1 ATGGCCAGGTGAAGCTGCGAGGAGCTGGACCTGAAGCTGGAGCGCTTTAGTG 60
Qy 66 LysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLys 85
Db 61 AATAATCTCGCAAGGCTTCTGGTTACCTTCACAGCTACGATATAAACTGGTGAG 120
Qy 86 GlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspPro 105
Db 121 CAGAGGCTCGACAGGAGCTTGTAGTGGATTGGATTTATCTCGAGATGGTAGTCT 180
Qy 106 SerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThr 125
Db 181 AAGTACAATGAGAAGTTCAAGGGCAGGCCACACTGACTGCAGACAAATCTCCAGCACA 240
Qy 126 AlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrCysAlaArg 145
Db 241 GCCTACATGCACTCAGCCGCTGACTCTGAGAACCTCTGAGACTTAATTTCTGTGCAAGA 300
Qy 146 SerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrVal 165
Db 301 GGG-----CAPAATTTGACTTCTGGGGCCAAAGGACACCGGTC 339
Qy 166 ThrValSerSerGlyGlyGlySerGlyGlySerGlyGlyGlyGlyGlySerAsp 185
Db 340 ACCGTCTCTCCAGTGAGCGGTTTCAGGGCGAGGTGGCTCTGGCGGTGGCGATCGGAC 399
Qy 186 IleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIle 205
Db 400 ATCGAGCTCACTCAGTCTCAGCTTCTTGGCTGTCTCTAGGCGAGGCGCACCATTA 459
Qy 206 SerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGln 225
Db 460 TCCTGCAGAGCCAGTGAAGTGTGATACTTATGGCGATACTTTTATGTACTGGTACCAG 519
Qy 226 GlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly 245
Db 520 CAGAAACCCAGGACGACCCCAACCTCTCATCTATCTTGCACACCACTTAGGATCTGGG 579
Qy 246 ValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspPro 265
Db 580 GTCCCTGCCAGGTTCATTGCGAGTGGTTAGCAGAACTTACCCCTCACCATCTGATCCT 639
Qy 266 ValGluGluAspAspAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThr 285
Db 640 GTGGGGCTGATGATGCTGCAACCTATTACTGTGAGCAAAATTAATGAGGATCGGTACAG 699
Qy 286 PheGlyGlyThrLysLeuGluIleLysArgAlaAlaSerGlySerGlyGlyGly 305
Db 700 TTCGAGGGGGCCCAAGCTGGAATCAACAT-----GGTGGAGGC 741
Qy 306 GlySer-----GlyGlyGlySerGlyGlyGly 314
Db 742 GGTTCACCATGGGGCCCGCTTCTCGCTGATCGCCGCTCGGGTCTGAGTGCAGGACAG 801
Qy 315 GlySerGlyGlyGlySerGlyAlaSerProValGln 327
Db 802 AGCGTGTGCGTGTGCGTACAGCGTGGCGCGCGCGGCGAG 840
```

RESULT 9

AAF30729 standard; DNA; 2190 BP.

XX AAF30729;
XX AC AAF30729;
XX DT 21-JUN-2001 (first entry)
XX DE Antibody 8860-alkaline phosphatase fusion DNA.
XX KW Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW alkaline phosphatase; ds.
XX OS Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX Key Location/Qualifiers
FH CDS 1..2190
FT /*tag= a
FT sig_peptide 1..66
FT /*tag= b
FT mat_peptide 67..2187
FT /*tag= c
XX WO200119992-A2.
XX PD 22-MAR-2001.
XX PF 13-SEP-2000; 2000WO-EP008936.
XX PR 14-SEP-1999; 99AT-00001576.
XX PA (BAXT) BAXTER AG.
XX Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX WPI; 2001-290358/30.
XX P-PSDB; AAB20439.
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX Example 16; Fig 29; 138pp; English.
XX The present sequence is that of DNA encoding a fusion protein (see
XX AAB20439) comprising (from the N-terminal end): a PeIB leader sequence; a
XX single chain Fv (scFv) derivative of antibody 8860 comprising the heavy
XX (VH) and light (VL) chain variable regions of antibody 8860 joined by an
XX artificial, flexible linker peptide; Escherichia coli alkaline
XX phosphatase; and a C-terminal 8His affinity tail. The DNA was used in the
XX construction of a miniantibody construct (see AAF30730), which was used
XX as a negative control in determination of Factor VIII (FVIII)-like activity
XX of a 198/B1 miniantibody. 198/B1 is an example of anti-human Factor IX
XX (FIX)/activated Factor IX (FIXa) antibodies of the invention. Anti-
XX FIX/FIXa antibodies and their derivatives have FVIIIa cofactor or FIXa
XX activating activity. Administration leads to an increase in the
XX procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors.
XX This allows for rapid blood coagulation even in the absence of FVIII or
XX FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
XX derivatives are used in a claimed pharmaceutical composition for treating
XX patients with blood coagulation disorders, especially haemophilia A and
XX haemorrhagic diathesis. The scFv-alkaline phosphatase was expressed in E.
XX coli. It exhibited no FVIII-like activity
SQ Sequence 2190 BP; 549 A; 579 C; 606 G; 456 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.14e-55 Length: 2190

Score:	993.50	Matches:	195
Percent Similarity:	83.85%	Conservative:	23
Best Local Similarity:	75.00%	Mismatches:	39
Query Match:	57.59%	Indels:	3
DB:	4	Gaps:	2
US-10-089-278-6 (1-329) x AAF30729 (1-2190)			
QY	41	AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg	60
Db	46	CGCGCCAGCCGCCATGGCCGAGGTTCAGTTTCAGCAGTCTGGACTGAGCTGGTGAAG	105
QY	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly	80
Db	106	CCCGGGCCCTCAGTGAAGATTTCTGCAGAACTTCTGGCTACGCATTCAGTACTCTGG	165
QY	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr	100
Db	166	ATGAACCTGGGTGAAGCAGAGCCCTGGACAGGGTCTTCAGTGGATTGGACGATTATCCT	225
QY	101	TyrTyrGlyAspProSerTyrAenGlnArgPheLysGlyLysAlaThrMetThrValAsp	120
Db	226	GGAAATGGAGATACTACATCAATGGAAGTTCAAGGCAAGCCACACTGACGAC	285
QY	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140
Db	286	ANATCTCCAGACAGCCTACATGACGCTCAGCAGCCTGACCTCTGTGACTCTCGGTC	345
QY	141	TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly	160
Db	346	TATTTCTGTGCA-----GATGTAACGTA--TATTACTATGCTATGACTACTGGGT	396
QY	161	GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly	180
Db	397	CAGGAACCTCAGTACCGTCTCTCAGGTGGAGCGGTTTCAGTGGCGCGCTCTGGC	456
QY	181	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly	200
Db	457	GGTGGCGGATCGCAATTTGTTCTCACCAGTCTCTCTCTCTCTCTCTCTCTCTCTCT	516
QY	201	GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe	220
Db	517	CAGAGGGCCACCATCTCATGACGGGCGCAGCAAAAGTGTCACTACATCTGGCTATAT	576
QY	221	MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer	240
Db	577	ATGCATCTGTATCCACAGAAACAGACAGCCACCCAACTCTCATCTATCTTGTATCC	636
QY	241	AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr	260
Db	637	AACCTAGATCTGGGTCTCCCTGCGAGTTTCAGTGGCAGTGGTCTGGACAGACTTCACC	696
QY	261	LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet	280
Db	697	CTCAACATCCATCTGTGGAGGAGGATGCTGCAACCTATTACTGTCTGACACAGTAGG	756
QY	281	GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAlaSer	300
Db	757	GAGTCTCTCGGAGTTCGGTGGAGGCCACCAAGCTGGAATCAACCGGCGCGCGAGCC	816
RESULT 10			
AAF30734			
ID	AAF30734 standard; DNA; 876 Bp.		
XX			
AC	AAF30734;		
XX			
DT	21-JUN-2001 (first entry)		
XX			
DE	DNA encoding antibody 8860 scFv with c-myc-tag.		
XX			
KW	Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;		
KW	Factor VIII cofactor; blood coagulation disorder; haemophilia A;		
KW	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag;		

KW	ds.
XX	Mus musculus.
OS	Synthetic.
OS	Escherichia coli.
OS	Chimeric.
XX	Key
FT	CDS
FT	1..876
FT	/tag= a
FT	sig_peptide
FT	1..86
FT	/tag= b
FT	mat_peptide
FT	67..873
FT	/tag= c
XX	WO200119992-A2.
XX	22-MAR-2001.
XX	13-SEP-2000; 2000WO-EP008936.
XX	14-SEP-1999; 99AT-00001576.
XX	(BAXT) BAXTER AG.
PA	Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;
PI	WPI: 2001-290358/30.
XX	P-PSDB; AAB20443.
DR	New factor IX/factor IXa antibodies and their derivatives useful for
XX	increasing amidolytic activity of factor IXa, and for treating blood
PT	coagulation disorders such as hemophilia A and hemorrhagic diathesis.
PT	Example 18; Fig 35; 138pp; English.
XX	The present sequence is that of DNA encoding a fusion protein (see
CC	AAB20443) comprising (from the N-terminal end): a PelB leader sequence; a
CC	single chain Fv (scFv) derivative of antibody 8860 comprising the heavy
CC	(VH) and light (VL) chain variable regions of 8860 joined by an
CC	artificial flexible linker peptide; a Myc-tag and a C-terminal 6His
CC	affinity tail. The fusion protein was expressed in Escherichia coli from
CC	vector pMylHis6. The construct was used as a negative control to
CC	determine the Factor VIII (FVIII)-like activity of a 198/B1 antibody scFv
CC	fragment (see AAB20442) also expressed from pMylHis6. 198/B1 (clone AB2)
CC	is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC	antibodies of the invention. Anti-FIX/FIXa antibodies and their
CC	derivatives, including scFv fragments, have FVIII cofactor activity or
CC	FIXa activating activity. Administration leads to an increase in the
CC	procoagulant activity of FIXa, even in the presence of FVIII inhibitors.
CC	This allows for rapid blood coagulation even in the absence of FVIII or
CC	FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
CC	derivatives are used in a claimed pharmaceutical composition for treating
CC	patients with blood coagulation disorders, especially haemophilia A and
CC	haemorrhagic diathesis
XX	Sequence 876 Bp; 211 A; 233 C; 239 G; 193 T; 0 U; 0 Other;
SQ	
Alignment Scores:	
Pred. No.:	5,44e-56
Score:	992.50
Percent Similarity:	83.78%
Best Local Similarity:	75.29%
Query Match:	57.54%
DB:	4
US-10-089-278-6 (1-329) x AAF30734 (1-876)	
QY	41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
Db	46 CGCGCCAGCCGCCATGGCCGAGGTTCAGTTTCAGCAGTCTGGACTGAGCTGGTGAAG 105
QY	61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80

Db	106	CCCCGGGCGCTCAGTGAAGATTCTCGCAAGCTTCTGGCTAGCATTCAGTACTCTTGG	165
Qy	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr	100
Db	166	ATGAACCTGGGTGAGCAGAGCGCTCGGACAGGGTCTTGAGTGGATTGGACGGATTATCTCT	225
Qy	101	TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyValSerLeuMetThrValasp	120
Db	226	GGAAATGGAGATACATACTAATGGGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC	285
Qy	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140
Db	286	AAATCTCTCCAGCAGACCTACATCAGCTCAGCAGCTGACCTCTGGGACTCTGCGGTC	345
Qy	141	TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly	160
Db	346	TATTTCTGTGCA-----GATGGTAACGTA---TATTACTATGCTATGGACTACTGGGT	396
Qy	161	GlnGlyThrThrValThrValSerGlyGlyGlySerGlyGlyGlyGlyGlySerGly	180
Db	397	CAGGAACCTCAGTCACCGTCTCTCAGGTGGAGCGGTTGAGTGGCGCGCTCTGGC	456
Qy	181	GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly	200
Db	457	GGTGGCGGATCGCAATTGTTCTCACCCAGTCTCTGCTCTCTTAGCTGTATCTCTGGG	516
Qy	201	GlnArgAlaThrIleSerCysArgAlaSerGlnSerValAspSerTyrGlyAspSerPhe	220
Db	517	CAGAGGCCACCATCTCATCGAGGCCAGCAAAAGTGTCTAGTATCTGGCTATAGTTAT	576
Qy	221	MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer	240
Db	577	ATGCACGTGGTACCAACAGAACAGGACAGCCAACTCTCATCTATCTTGTGCATCC	636
Qy	241	AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr	260
Db	637	AACTAGATCTGGGTCTCTCCAGGTTTCAGTGGCAGTGGTCTGGCAGACAGATTCCAC	696
Qy	261	LeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGlnSerMet	280
Db	697	CTCAACATCCATCTCTGGAGGAGGAGGAGTCTGCAACCTATTACTGTGCAGCAGTAGG	756
Qy	281	GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla	299
Db	757	GAGCTTCTCGGACGTTCTGGTGGAGCACCAGCTGGAAATCAAAACGGCGCGCA	813
RESULT 11			
AAF30730			
ID	AAF30730	standard; DNA; 969 BP.	
XX	AC	AAF30730;	
XX	21-JUN-2001	(first entry)	
XX	Antibody	8860 bivalent miniantibody DNA.	
XX	Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;		
XX	Factor VIII cofactor; blood coagulation disorder; haemophilia A;		
XX	haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;		
XX	bivalent antibody; p8860-Zip#1.2; ds.		
OS	Mus musculus.		
OS	Synthetic.		
OS	Escherichia coli.		
OS	Chimeric.		
PH	Key	Location/Qualifiers	
FT	CDS	1..969	
FT		/*tag= a	
FT	sig_peptide	1..66	
FT		/*tag= b	
FT		/note= "PelB leader sequence"	

FT	mat_peptide	67..966	
FT		/*tag= c	
XX	WO200119992-A2.		
XX	22-MAR-2001.		
XX	13-SEP-2000; 2000WO-EP008936.		
XX	14-SEP-1999; 99AT-00001576.		
XX	(BAXT) BAXTER AG.		
XX	Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;		
XX	WPI; 2001-290358/30.		
XX	P-PSDB; AAB20440.		
XX	New factor IX/factor IXa antibodies and their derivatives useful for		
XX	increasing amidolytic activity of factor IXa, and for treating blood		
XX	coagulation disorders such as hemophilia A and hemorrhagic diathesis.		
PS	Example 16; Fig 30; 138pp; English.		
XX	The present sequence is that of the coding region of plasmid p8860-		
XX	Zip#1.2 encoding a bivalent miniantibody (see AAB20440) comprising the		
XX	single chain Fv (scFv) fragment of antibody 8860 fused to an amphipathic		
XX	helic structure. The plasmid was obtained by inserting 8860 scFv DNA		
XX	into vector pZipl. The construct was used as negative control in		
XX	examination of the Factor VIII (FVIII)-like activity of an antibody		
XX	193/B1 miniantibody (see AAB20438). 193/B1 is an example of an anti-human		
XX	Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.		
XX	Anti-FIX/FIXa antibodies and their derivatives have FVIII cofactor		
XX	activity or FIXa activating activity. Administration leads to an increase		
XX	in the procoagulant activity of FIXa, even in the presence of FVIIIa		
XX	inhibitors. This allows for rapid blood coagulation even in the absence		
XX	of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The		
XX	antibodies and derivatives are used in a claimed pharmaceutical		
XX	composition for treating patients with blood coagulation disorders,		
XX	especially haemophilia A and haemorrhagic diathesis. The present bivalent		
XX	miniantibody exhibited no FVIII-like activity		
SQ	Sequence 969 BP; 233 A; 257 C; 264 G; 215 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	6e-56	Length:	969
Score:	992.50	Matches:	195
Percent Similarity:	83.78%	Conservative:	22
Best Local Similarity:	75.29%	Mismatches:	39
Query Match:	57.54%	Indels:	3
DB:	4	Gaps:	2
US-10-089-278-6 (1-329) x AAF30730 (1-969)			
Qy	41	AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg	60
Db	46	CGCGCCAGCGCGCCATGGCGAGGTTACGTTTCAGAGCTCGAGCTGGTGAAG	105
Qy	61	ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly	80
Db	106	CCCGGGCCCTCAGTGAAGATTCTCTGCAAAAGCTTCTGGCTACGCATTCAGTACTCTGG	165
Qy	81	MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr	100
Db	166	ATGAACCTGGGTTGAAGCAGAGCGCTGGAGTGGGCTTGGAGTGGATTCGATTCCT	225
Qy	101	TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyValSerLeuMetThrValasp	120
Db	226	GGAAATGGAGATACATACTAATGGGAAGTTCAAGGGCAAGGCCACACTGACTGCAGAC	285
Qy	121	LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle	140
Db	286	AAATCTCTCCAGCAGCCTACATCAGCTCAGCAGCTGACCTCTGGGACTCTGCGGTC	345

QY 141 TTTTCTGTCGCA-----GATGTAACGTA---TATTACTATGCTATGACTACTGGGT 396
 Db
 QY 161 GlnGlyThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
 Db 397 CAAGGAACCTCAGTCAACCGTCTCTCAGGTGGAGCGGTTCAGGTGGCGCGCTCTGGC 456
 QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
 Db 457 GGTGGCGGATCGCAAAATTGTTCTCACCCAGTCTCTCTCTAGCTGTATCTCTGGG 516
 QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
 Db 517 CAGAGGCCACCATCTCATGCGGGCGCAGCAAGATGTCAGTACATCTGGCTATAGTTAT 576
 QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
 Db 577 ATGCACTGGTACCAACAGAAACCAGACAGCCACCCCAAACTCTCATCTATCTTGCATCC 636
 QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
 Db 637 AACCTAGAATCTGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACC 696
 QY 261 LeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
 Db 697 CTCACATCATCTCTGTGGAGGAGGATGCTGCAACCTATTACTGTCTAGCAGATAGG 756
 QY 281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 299
 Db 757 GACCTTCCTCGGACGTTCCGTGGAGGAGGATGCTGCAACCTATTACTGTCTAGCAGATAGG 813
 RESULT 12
 ADS88776
 ID ADS88776 standard; DNA; 897 BP.
 XX
 AC ADS88776;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Nucleotide sequence of the IC2 scFv antibody from clone p530.
 XX
 KW G glycoprotein; respiratory syncytial virus;
 KW respiratory syncytial virus infection; RSV; RSV infection; IC2; scFv;
 KW gene; ds.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..897
 FT /*tag= b
 FT /product= "IC2 scFv"
 FT sig_peptide 1..66
 FT /*tag= a
 FT /note= "PelB leader sequence"
 XX
 PN WO2004083373-A2.
 XX
 PD 30-SEP-2004.
 XX
 PF 22-MAR-2004; 2004WO-GB001239.
 XX
 PR 22-MAR-2003; 2003GB-00006618.
 XX
 PA (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
 XX
 PI Toms G, Routledge E, Mekseepalard C;
 XX WPI; 2004-691033/67.
 DR P-PSDB; ADS88777.
 XX

PT New antibody against the G glycoprotein of RSV with a variable region
 PT having a first and second domain from a VL and VH region, respectively,
 PT useful for treating respiratory syncytial virus (RSV) infections.
 XX Example 2; SEQ ID NO 44; 93pp; English.
 PS
 XX The specification describes an against the G glycoprotein of respiratory
 CC syncytial virus, with a variable region comprising a first domain from a
 CC variable light chain region and a second domain a variable heavy chain
 CC region. The antibodies of the invention are useful for treating and
 CC preventing the development of infections caused by the respiratory
 CC syncytial virus (RSV). The present sequence encodes the IC2 scFv from
 CC clone p530. This scFv is an exemplary antibody of the invention. IC2 is a
 CC murine monoclonal antibody known to bind to the SV G glycoprotein. IC2
 CC was used as a source of sequences to construct antibodies of the
 CC invention.
 XX
 SQ Sequence 897 BP; 224 A; 215 C; 251 G; 207 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,97e-56 Length: 897
 Score: 991.00 Matches: 191
 Percent Similarity: 83.85% Conservative: 27
 Best Local Similarity: 73.46% Mismatches: 40
 Query Match: 57.45% Indels: 2
 DB: 13 Gaps: 2
 US-10-089-278-6 (1-329) x ADS88776 (1-897)
 QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
 Db 46 GCGGCCCGCCGCCATGGCCAGGTGCGAGTGCAGCAGTCAGGGCTCAGGTGGTGGAG 105
 QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
 Db 106 CCTGGGGTCTCGCGAGGATTTCTCTCAAGGGATTCGGCTACACATTCATCTAGTATGCT 165
 QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
 Db 166 ATGCACTGGTGAAGCAGAGTCCGCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACT 225
 QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
 Db 226 TACTATGTTAATCAAAATTACAACCAAGAGTTTAAGGCAAGGCCACAATGACTGTAGAC 285
 QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaAArgLeuThrSerGluAspSerAlaIle 140
 Db 286 AAATCCTCCAGCACAGCCTATATGGAACCTTGACATATGAGGATTCGCAATCTGCATC 345
 QY 141 TyrTyrCysAlaArgSerAspGly---AsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrp 159
 Db 346 TATTACTGTGCAAGATCGATATGATTACGGCGCGCGGGGTATGCTATGGACTACTGG 405
 QY 160 GlyGlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySer 179
 Db 406 GGCACAGGACACACGGTCCACCGTCTCCAGTGTGGAGCGGGTTTCAGCGGAGGTGCTCT 465
 QY 180 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeu 199
 Db 466 GCGGTAGTGGCACAGGATGTTTGTAGACCCAGACTCCTCTCTCCCTGCTGCTGCTT 525
 QY 200 GlyGlnArgAlaThrIleSerCysArgAlaSerGluSer---ValAspSerTyrGlyAsp 218
 Db 526 GGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAACATGTACATAGTGTGAAAC 585
 QY 219 SerPheMetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArg 238
 Db 586 ACCTATTAGAGTGTACCTTCAGAGAACCCAGGCGAGTCTCCAAAGCTCTCTGATCTACAA 645
 QY 239 AlaSerAsnLeuGluSerGlyValProAlaAArgPheSerGlySerGluSerAsp 258
 Db 646 GTTTCACACCGATTTTCTGGGGTCCAGACAGGTTCATGTCGAGTGGATCGGACAGAT 705

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QY 259 PheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrCysLeuGln 278
DB 706 TTCACACTCAAGATCAGCAGGTGGAGCTGGAGTCTGGAGTTTATTACTGCTTCAA 765

QY 279 SerMetGluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAla 298
DB 766 GGTTCACATATTCGTGGACGTTGGTGGAGGGACCAAGCTGGAGATCTCCGGCGCGCA 825

RESULT 13
AAZ43431
ID AAZ43431 standard; DNA; 1698 BP.
XX
AC AAZ43431;
DT 18-FEB-2000 (first entry)
XX
DE Fv-antibody construct containing antibody 9E10 epitope DNA.
XX
KW Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
KW diagnosis; therapy; disease; ss.
XX
OS Synthetic.
XX
PN DE19819846-A1.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1998; 98DE-01019846.
XX
PR 05-MAY-1998; 98DE-01019846.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Little M, Kipriyanov S;
XX
DR WPI; 2000-024472/03.
XX
P-PSDB; AAY50822.
XX
PT Multivalent Fv-antibody constructs with at least four variable domains
PT connected by 1, 2 and 3 peptide linkers.
XX
PS Example 1; Fig 5; 14pp; German.
XX
CC This invention describes a novel multivalent Fv-antibody construct with
CC at least four variable domains that are connected to one another by 1, 2
CC and 3 peptide linkers. The construct has antiviral, antibacterial and
CC cytostatic activity. The multivalent Fv-antibody constructs are useful
CC for the diagnosis and/or therapy of disease, especially viral, bacterial
CC or tumor diseases. The multivalent Fv-antibody constructs have increased
CC stability when in the form of a single chain dimer. This sequence encodes
CC a bivalent Fv antibody construct composed of the antibody 9E10 epitope in
CC expression plasmid pDISC3x19-L1.
XX
SQ Sequence 1698 BP; 433 A; 434 C; 450 G; 381 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 13e-55 Length: 1698
Score: 991.00 Matches: 197
Percent Similarity: 80.50% Conservative: 30
Best Local Similarity: 69.86% Mismatches: 45
Query Match: 57.45% Indels: 10
DB: Gaps: 3

US-10-089-278-6 (1-329) x AAZ43431 (1-1698)

QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
DB 73 GCAGCTCAGCCGCCATGGCGCAGGTGCACACTGCAGCAGTCTGGGCTGAACTGGCAAGA 132

QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
DB 133 CTTGGGGCCTCAGTGAAGATGTCTCGAAGGCTTCTGGCTACACCTTTTACTAGGTACACG 192

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QY 81 MetSerTyrValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
DB 193 ATGCACCTGGGTAAACAGAGGCTGCAGAGGCTCTGGATGGATTGGATACATTATTCCT 252

QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
DB 253 AGCCGTGGTTTATTAATAATCAATCAGAACTTCAAGGACAAGCCACATTGACTACAGAC 312

QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
DB 313 AAATCCTCCAGCACAGCCTACATGCACTGAGCAGCCTGCACATCTGAGGACTCTGCAGTC 372

QY 141 TyrTyrCysAlaAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160
DB 373 TATTACTGTGCAAGA-----TATTATGATGATCATTTACAGCCTTGTACTCTGGGGC 423

QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlyLysSerGlyGlyGlySerGly 180
DB 424 CAAAGGCACCACTCTCAGACTCTCTCAGCCAAACAACACCCCAAGCTTGGCGGT----- 477

QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
DB 478 -----GATATCTTGTCTCACCCAAACTCCAGCTTCTTTGGCTGTGTCTTAGGG 525

QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
DB 526 CAGAGGGCCACCACTCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGATAGTTAT 585

QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240
DB 586 TTGAACCTGGTACCACAGATTCAGGACAGCCACCCAACTCCTCATCTATGATGATCATCC 645

QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
DB 646 AATCTAGTTTCTGGGATCCACCCAGCTTGTAGTGGCAGTGGGTCTGGGACAGACTTCACC 705

QY 261 LeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
DB 706 CTCACATCCATCTCTGTGGAGAAGTGGATGTGCAACCTATCCTGTCAGCAAAAGTACT 765

QY 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaAsp 300
DB 766 GAGGATCCGTGGAGCTTGGTGGAGGCCACCAAGCTGAAATCAACGGGCTGATGCTGCG 825

QY 301 GlySerGlyGlyGlyGlySer---GlyGlyGlySerGlyGlyGlySerGlyGlyGly 319
DB 826 GCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 885

QY 320 GlySer 321
DB 886 GGTAGC 891

RESULT 14
AAZ44206
ID AAZ44206 standard; DNA; 925 BP.
XX
AC AAZ44206;
DT 31-MAR-2000 (first entry)
XX
DE Murine derived DNA fragment #4.
XX
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine; ds.
XX
OS Mus sp.
XX
PN WO9961629-A1.
XX
PD 02-DEC-1999.
XX
PF 24-MAY-1999; 99WO-JP002711.

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XX 25-MAY-1998; 98JP-00159957.
PR 26-MAY-1998; 98JP-00163023.
XX
XX (ASAH ) ASahi KASEI KOGYO KK.
PA (ASAH ) ASahi MEDICAL CO LTD.
XX
XX Ono M, Soka T, Morimoto I, Miyamura K;
PI
XX WPI; 2000-086720/07.
DR P-PSDB; AAY51142.
XX
XX Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells.
PT
XX Claim 22; Page 82-84; 11pp; Japanese.
XX
XX This invention describes a novel device (I) for separating cluster
CC differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for the
CC collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal compositions
CC for the treatment of HIV infection and autoimmune diseases. This sequence
CC encodes a murine derived protein fragment which is used to illustrate the
CC method of the invention
XX
XX SQ Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,38e-55 Length: 925
Score: 983.00 Matches: 189
Percent Similarity: 83.33% Conservative: 26
Best Local Similarity: 73.26% Mismatches: 39
Query Match: 56.99% Indels: 4
DB: 3 Gaps: 1

US-10-089-278-6 (1-329) x AAZ44206 (1-925)
QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
DB 46 GCGGCCAGCGCGGCATGGCCAGGTTTCAGTCGAGCAGTCTGGACCTCGAGCTGGTGAAG 105
QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyThrPheThrAspTyrGly 80
DB 106 CCGGGGCTTCAGTGAAGATGCTCTGCAAGGCTTCGTGATACACATCTCACTGACTAGTT 165
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
DB 166 ATAACTGGTTGAACACAGAACTGGACAGGCGCTTGAGTGGATGGAGAGATTATCCT 225
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
DB 226 GGAAGTGGTAGTGTTACTACATAGATGTTCAAGGGCAAGCCACACCTGACTGCAGAC 285
QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
DB 286 AAATCTCCCAACACAGCCTATACAGCTCAGCAGCCTGACATCTGAGGACTCTGCCGTC 345
QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
DB 346 TATTTCTGTCAGACCGGNACTGGGACGGGTTT-----GCTTACTGGGC 393
QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
DB 394 CGAGGAGCTCTGGTCACTGTCTCTGAGGTGGAGCGGTTTCAGCGCAGGTGGCTCCGGA 453
QY 181 GlyGlyGlySerAlaGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
DB 454 GGTGGCGGATCGGACATGTGCTGACCAATCTCCAGCTCTTTGGCTGTCTTAGGG 513
QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220

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DB 514 CAGAGGGCCACCATCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGATAGTTAT 573
QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240
DB 574 ATGAACTGGTACCAACAGAAACAGGACAGCCACCAAACTCCTCATCTATGCTGCATCC 633
QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
DB 634 AATCTAGAATCTGGGATCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACC 693
QY 261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280
DB 694 CTCACATCATCTCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCTCAGCAAGTAGT 753
QY 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaIle 298
DB 754 GAGGATCTCCAGCGTTCGGTGGAGCCACCAAGCTGGAATCAAGCGGCCGCA 807

RESULT 15
AAZ58664
ID AAZ58664 standard; cDNA to mRNA; 925 BP.
XX
XX AAZ58664;
XX AC
XX DT 17-APR-2000 (first entry)
XX DE Antibody 4H5 L chain encoding nucleotide sequence.
XX KW CD4 antigen; anti-human; antibody; 4H5; drug; ds.
XX OS Mus sp.
XX PN JP11332563-A.
XX PD 07-DEC-1999.
XX PF 26-MAY-1998; 98JP-00163034.
XX PR 26-MAY-1998; 98JP-00163034.
XX PA (ASAH ) ASahi KASEI KOGYO KK.
XX DR WPI; 2000-091351/08.
XX DR P-PSDB; AAY59265.
XX PT An antibody and the nucleic acid coding the antibody.
XX PS Disclosure; Page 17-18; 25pp; Japanese.
XX CC The invention provides an antibody having affinity to CD4 antigen. The
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
XX application for drugs. It is highly safe in human dose. The present
XX sequence represents the antibody 4H5 L chain encoding nucleotide sequence
SQ Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,38e-55 Length: 925
Score: 983.00 Matches: 189
Percent Similarity: 83.33% Conservative: 26
Best Local Similarity: 73.26% Mismatches: 39
Query Match: 56.99% Indels: 4
DB: 3 Gaps: 1

US-10-089-278-6 (1-329) x AAZ58664 (1-925)
QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
DB 46 GCGGCCAGCGCGGCATGGCCAGGTTTCAGTCGAGCAGTCTGGACCTCGAGCTGGTGAAG 105
QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyThrPheThrAspTyrGly 80

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Db 106 CCTGGGGCTTCAGTGAAGATGCTCTGCAAGGCTTCTGGATACACATTCACTGACTATGTT 165
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 166 ATAAACTGGTTGAACACAGAACTGGACAGGGCCCTTGAGTGGATTGGAGAGATTATCCT 225
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 GGAAGTGGTAGTCTTACTACATGAGATGTTCAAGGGCAGGCCACACTGACCTGCAGAC 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AATCCTCCAAACAGCCTACATGCAGCTCAGCAGCCCTGACATCTGAGGACTCTGCCGCTC 345
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
Db 346 TATTTCGTGTCAGACCGGAACCTGGGACGGGGTTT-----GCTTACTGGGGC 393
Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGly 180
Db 394 CGAGGGACTCTGGTCACTGTCTCTGCAGGTGGAGCGGTTTCAGCGGAGGTGGCTCCGA 453
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 454 GGTGGCGGATCGGACATTGTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGG 513
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
Db 514 CAGAGGGCCACCATCTCTCGCAGGCCAGCCAAAGTGTGATTATGATGGTGTAGTTAT 573
Qy 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
Db 574 ATGAACTGGTACCAACAGAACCCAGGACGCCCAACTCCTCATCTATGCTGCATCC 633
Qy 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 634 AATCTAGAATCTGGGATCCCGAGCCAGGTTTAGTGGCAGTGGTCTGGGACAGACTTCACC 693
Qy 261 LeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
Db 694 CTCAACTCCATCCTGTGGAGGAGGAGATGCTGCAACCTATTACTGTGCAAAAGTAGT 753
Qy 281 GluAspProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAla 298
Db 754 GAGGATCTCCGACGTTCCGGTGGAGGCCCAAGCTGGAATCAAAAGCGCCGCA 807

Search completed: August 23, 2005, 14:42:30
Job time : 548 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 13:50:35 ; Search time 3106 Seconds
(without alignment)
4031.920 Million cell updates/sec

Title: US-10-089-278-6
Perfect score: 1725
Sequence: 1 MDCLTNLSAEKVDQASKI.....GSGGGSGGGSGASPVQFI 329

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEX=6 -DELEXT=7

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2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gse1.*
9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	761	44.1	671	3 AF240168	AF240168 Mus muscu
C 2	671	38.9	872	7 CK629396	CK629396 AMO-AA001
C 3	668	38.7	601	5 BQ474958	BQ474958 carabus4g
C 4	645	37.4	1104	7 CK629846	CK629846 AM2-AR002
C 5	638	37.0	1339	7 CK629414	CK629414 AM1-AA001
6	631.5	36.6	672	7 CK633068	CK633068 AM3-AP001
7	631.5	36.6	672	7 CK633069	CK633069 AM3-AP001
C 8	631	36.6	535	3 AF240170	AF240170 Mus muscu
9	631	36.6	540	3 AF240167	AF240167 Mus muscu

C 10	629.5	36.5	1419	7	CK629415	CK629415 AM1-AA001
C 11	602	34.9	823	7	CK632348	CK632348 AMO-AM000
C 12	599	34.7	683	3	AF240172	AF240172 Mus muscu
13	523	30.3	407	2	AW988429	AW988429 ug08d07.y
14	520.5	30.2	565	2	BF801321	BF801321 MR0-CI002
15	511.5	29.7	738	4	BG965088	BG965088 602829160
16	510	29.6	327	4	BG148320	BG148320 uu91c06.y
C 17	505.5	29.3	567	5	BQ328142	BQ328142 MR4-RT004
C 18	505.5	29.3	963	7	CK629843	CK629843 AM2-AA002
C 19	503.5	29.2	489	2	BF855922	BF855922 PM2-FN021
20	503	29.2	544	5	BQ310337	BQ310337 MR0-BT450
21	500	29.0	732	4	BG962768	BG962768 602830291
22	498	28.9	750	4	BG965050	BG965050 602829112
23	498	28.9	876	4	BI107286	BI107286 602894285
24	492.5	28.6	453	5	BQ346956	BQ346956 PM2-NT016
25	489.5	28.4	504	2	BF759134	BF759134 MR0-CT054
26	489.5	28.4	577	1	AJ548139	AJ548139 AJ548139
27	486.5	28.2	569	2	BF842604	BF842604 MR0-HT092
28	483.5	28.0	527	2	BF921283	BF921283 PM2-NT016
29	478.5	27.7	626	7	CK632177	CK632177 AM1-AM000
30	478	27.7	598	4	BI104341	BI104341 602889919
31	475	27.5	599	5	BQ310276	BQ310276 MR0-BT250
32	469.5	27.2	490	4	BI050614	BI050614 PM1-GN040
33	469	27.2	922	2	BF584560	BF584560 602098269
34	468.5	27.2	507	2	BF015548	BF015548 uy23a08.y
C 35	468	27.1	585	4	BI030095	BI030095 IL0-MT035
C 36	467	27.1	653	5	BQ321980	BQ321980 MR1-CT073
37	466	27.0	643	6	BY733441	BY733441 BY733441
38	465.5	27.0	442	5	BQ342972	BQ342972 PM0-NN022
39	463	26.8	569	7	CK332703	CK332703 H821OE01-
40	463	26.8	831	4	BG966589	BG966589 602834422
41	460	26.7	685	2	BF136104	BF136104 601783550
42	460	26.7	806	4	BI108506	BI108506 602894952
43	458.5	26.6	465	6	CA578116	CA578116 K0718G11-
44	458	26.6	774	2	BF581989	BF581989 602099444
45	457	26.5	926	2	BF787780	BF787780 602113542

ALIGNMENTS

RESULT 1	AF240168	671 bp	mRNA	linear	HTC 30-APR-2001
LOCUS	AF240168	Mus musculus MRP5 mRNA, partial cds.			
DEFINITION	AF240168				
ACCESSION	AF240168.1	GI:13877288			
VERSION	HTC				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 671)				
AUTHORS	Cui, D.X., Zeng, G.Y., Wang, F., Xu, J.R., Ren, D.Q., Guo, Y.H., Tian, F.R., Yan, X.J., Hou, Y., and Su, C.Z.				
TITLE	Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice				
JOURNAL	World J. Gastroenterol. 6 (5), 709-717 (2000)				
PUBMED	11819679				
REFERENCE	2 (bases 1 to 671)				
AUTHORS	Cui, D., Zeng, G., Yan, X., Li, X. and Su, C.				
TITLE	Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain				
JOURNAL	Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80 (2001)				
REFERENCE	3 (bases 1 to 671)				
AUTHORS	Cui, D., Zeng, G., Yan, X., Wang, F., Tian, F., Ren, D., Zhao, T., Li, X. and Su, C.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China				
FEATURES	Location/Qualifiers				

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source
1. .671
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/sex="male"
/cell_type="intestinal gland cell"
/notes="derived from differential display PCR between
irradiated mice with and without RNA injection"
18. .>671
/notes="related to the repair of irradiation-damaged
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/codon_start=1
/product="WRP5"
/protein_id="AAK43733.1"
/db_xref="GI:13877289"
/translacion="MAQVQLQQSQPELKPGETVRIACKASGYFTFTAGMQVQKMG
KGLKGIWINTHSVPKYAEFKRFAFLETSATYLOISLNKNDTATYFCMRWD
YDGFAYVGGGTTVTSSGGSGGGSGGSDIVLTQSPASLAVSLGORATISCPA
SESVDNIGISPMWVQKPGPPKLLIYAASKQSGVPGALLSGSGTDFSLIYPME
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ORIGIN
Alignment Scores:
Pred. No.: 1.09e-60 Length: 671
Score: 761.00 Matches: 148
Percent Similarity: 78.85% Conservative: 31
Best Local Similarity: 65.20% Mismatches: 44
Query Match: 44.12% Indels: 4
DB: 3 Gaps: 1

US-10-089-278-6 (1-329) x AF240168 (1-671)
Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnInSerGlyAlaGluLeuValArg 60
Db 3 GCGGCCAGCGCGCATGCCCGAGTGAACAGTGCAGCAGTGCAGCAGTGAACAGGAG 62
Qy 61 ProGlyValSerValLysLeuSerCysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 63 CCTGGAGAGACGTCAGTATCTCTGCAGGCTTCTGGATATACCTTCACAACTGCTGGA 122
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuLeuSerThr 100
Db 123 ATGCAGTGGTGCAGAGATCCAGGAAGAGGTTGAAGTGGATGGCTGATTAACACC 182
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 183 CACTCTGGAGTGCAGAGATATGCAGAGATTCAGGAGCGCTTTGCCCTTCTCTTTGGAA 242
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 243 ACCTCTGCCAGCATGCATATTTACAGATAGAACCTCAAAATATGAGGACCGCTACG 302
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGly 160
Db 303 TATTCTGTATGAGATGGATATACACGGGGGTTT-----GCTTACTGGGCG 350
Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
Db 351 CAAGGGACACCGGTCCCGTCTCTCAGTGGAGCGGTTTCAGGCGGAGGTGGCTTGGC 410
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 411 AGTGCGGATCGGACATCGTCTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGG 470
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
Db 471 CAGAGGGCCACCATCTCTCGCAGACGACGAGAAAGTGTGTGATAATATATGGCATAGTTT 530
Qy 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSer 240
Db 531 ATGAACCTGGTCCAGCAGAAACAGGACGACCCCAACCTCCTCATCTATGCTGCATCC 590

RESULT 2
CK629396/c
LOCUS CK629396 872 bp mRNA linear EST 26-MAR-2004
DEFINITION AMO-AA0013-110902-011-H03 AA0013 Apis mellifera cDNA, mRNA
sequence.
VERSION CK629396.1 GI:45753871
KEYWORDS Apis mellifera (honey bee)
SOURCE Apis mellifera
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
REFERENCE 1 (bases 1 to 872)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreatico,E.M.,
Bepindota,F.S., Pado-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
CONTACT: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonj@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 66
High quality sequence stop: 625.
FEATURES
source
1..872
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_lib="AA0013"
/notes="Organ: whole body"

ORIGIN
Alignment Scores:
Pred. No.: 3.79e-52 Length: 872
Score: 671.00 Matches: 137
Percent Similarity: 73.62% Conservative: 36
Best Local Similarity: 58.30% Mismatches: 50
Query Match: 38.90% Indels: 15
DB: 7 Gaps: 3

US-10-089-278-6 (1-329) x CK629396 (1-872)
Qy 65 vallysleSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpVal 84
Db 775 ATGAATATGCTCTCAAGCT-TCTGC-TACATCTCAAGTTATGATATAGACTGGGTG 718
Qy 85 LysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuLeuSerThrTyrTyrGlyAsp 104
Db 717 AGGCAGACGCTGACAGGAGCTTGGTGGATGGATG-GTTTTCTCGAGAGGGAGT 659
Qy 105 ProSerTyrAsnGlnA-gPheLysGlyLysAlaThrMetThrValAspLysSerSerAsn 124

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658 ACTGAATACAAATGAGAAGTTCAAGGCGAGGCCACACACTGAGTGTAGACAGTCTCCAGC 599
 125 ThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAla 144
 598 ACAGCCTATATGAGGCTCACTAGGCTGACATCTGAGGACTCTGCTGTCTATTCTGTGCT 539
 145 ArgSerAspGlyAsnTyrGlyTyrTyrTyrAla-----LeuAspTyrTrpGlyGlnGly 162
 538 AGAGGGGAC-----TACTATAGGCGGTACTTTGACTGTGGNCCAGGG 494
 163 ThrThrValThrValSerGlyGlyGlyGlySerGlyGlyGlyGlyGlyGlyGlyGly 182
 493 ACCACGGTCACTCTCTCTCATGTGAGCGGTTCAGGCGGAGTGGCTCTGCGGTGC 434
 183 GlySerAspIleLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArg 202
 433 GGATCTTGACATTGAGCTCACTGAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAG 374
 203 AlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHis 222
 373 GTCACCATGACCTGCAGTGCAGCTCAAGTATATA-----CGTTACATATAT 329
 223 TrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeu 242
 328 TGGTACCAACAGAGCTGGATCTCTCCAGGACTCTGTATTTATGACATCCACAGTG 269
 243 GluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThr 262
 268 GCTCTCGAGTCCCTTTTTCGCTTCACTGCGAGTGGGTCTGGACCTCTTATTTCTTCACA 209
 263 IleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMetGluAsp 282
 208 ATCAACCGAATGAGGCTGAGGATGCTGCCATTTATCTGCCAGGAGTGGAGTGGTTAT 149
 283 ProTyrThrPheGlyGlyThrLysLeuGluIleLysArgAla 297
 148 CCGTACACGTTCCGAGGGGGACCAAGCTGGAGCTGAACCGGGCG 104
 RESULT 3
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 FEATURES
 source

Alignment Scores:
 Pred. No.: 4,39e-52 Length: 601
 Score: 668.00 Matches: 129
 Percent Similarity: 75.71% Conservative: 30
 Best Local Similarity: 61.43% Mismatches: 39
 Query Match: 38.72% Indels: 12
 DB: 5 Gaps: 3
 US-10-089-278-6 (1-329) x BQ474958 (1-601)
 QY 90 LysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyrAsnGln 109
 DB 601 CAGGAGCTTGAAGTGGATGGATGGATTTTCTCTGGAGAGGAGTACTGAATACATAGAG 542
 QY 110 ArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyrLeuGlu 129
 DB 541 AAGTTCAAGGGCAGGGCCACACTGAGTGTAGACAGTCTCTCCAGCACACCTATATGGAG 482
 QY 130 LeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAspGlyAsn 149
 DB 481 CTCACCTAGGCTGACATCTGAGGACTCTGCTGTCTATTCTGTCTAGAGGGGAC----- 428
 QY 150 TyrGlyTyrTyrTyrAla-----LeuAspTyrTrpGlyGlnGlyThrThrValThrVal 167
 DB 427 -----TACTATAGGCGGTACTTTGACTTTGTGGGCGCAAGGGACCAAGGTCACCGTC 377
 QY 168 SerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlyGlySerAspIleGlu 187
 DB 376 TCCTCATGTGGAGCGGTTCAGGCGGAGTGGCTCTGGCGGTGGCGATCTGCATTTGAG 317
 QY 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
 DB 316 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACCATGACCTGC 257
 QY 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLys 227
 DB 256 AGTGCAGCTCAAGTATA-----CGTTACATATATTGGTACCACAGAG 212
 QY 228 ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
 DB 211 CTTGGATCTCTCCAGGACTCTGTATTTATGACATCCACAGTGGCTCTCTGGAGTCCCT 152
 QY 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
 DB 151 TTTTCGCTTCACTGCGAGTGGGTCTGGGACCTCTTATCTCTCAATCAACCGCAATGGAG 92
 QY 268 GluAspAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
 DB 91 GCTGAGGATGCTGCCACTTATTTACTGCCAGGAGTGGAGTGGTTATCCGTACACGTTCCGA 32
 QY 288 GlyGlyThrLysLeuGluIleLysArgAla 297
 DB 31 GGGGGGACCAAGCTGGAGCTGAACCGGGCG 2
 RESULT 4
 BQ474958/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 FEATURES
 source

Ramos,R.G.P., Reis,L.F.L, Dias Neto,E., Souza,S.J., Simpson,A.J.G., Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M., Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and Silva,W.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome

Unpublished (2004)

Contact: Silva Jr, W. A.

Molecular Genetic and Bioinformatics Laboratory

Department of Genetics, FMRP/USP, FUNDHERP

Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 39639300

Fax: +55 16 39639309

Email: wilsonjr@usp.br

This sequence was derived from the FAPESP Genome Program

High quality sequence start: 64

High quality sequence stop: 594.

Location/Qualifiers

1. .1104

/organism="Apis mellifera"

/mol_type="mRNA"

/strain="Africanized"

/db_xref="taxon:7460"

/sex="female, worker"

/dev_stage="adult"

/clone_lib="AA0023"

/note="Organ: whole body"

ORIGIN

Alignment Scores:

Pred. No.: 1.38e-49 Length: 1104

Score: 645.00 Matches: 139

Percent Similarity: 71.31% Conservative: 35

Best Local Similarity: 56.97% Mismatches: 55

Query Match: 37.39% Indels: 17

DB: 7 Gaps: 4

US-10-089-278-6 (1-329) x CK629846 (1-1104)

QY 57 GluLeuValArgProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPhe 76

DB 783 GAATTCGTAAAGCTCGGGCTTCAAT---GANTTTCTCGCAGGCT-TCTTGTCATCTTC 728

QY 77 ThrAspTyrGlyMetSerTrpValLysGlnSerHisAla-LysSerLeuGluTrpIleG1 96

DB 727 ACAAGTTATCATATAGACTGGTTGAGCGACGCCCTGAACAAGGACTTGAGTGATGG 668

QY 96 YLeuIleSerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaTh 116

DB 667 ATGGATTTTCTCGAGAGGGAGTACTGAATACATGAAAGTTCAAGGGCAGGCAAC 608

QY 116 rMetThrValAspLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerG1 136

DB 607 ACTGAGTGTAGACAAGTCTCCAGCAGCAGCTATATGGAGCTCCTCAGGCTGACATCTGA 548

QY 136 uAspSerAlaIleTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAla-- 155

DB 547 GGACTCTGCTCTATTCTCTGCTAGAGGGAC-----TACTATAGGCG 503

QY 156 ----LeuAspTyrTrp-GlyGlnGlyThrThrValThrValSerSerGlyGlyGlys 174

DB 502 CTACTTTGACTTGTGGGGCCAAAGGACCACCGTCTCCTCATGTGGAGCGGTT 443

QY 174 erGlyGlyGlySerGlyGlyGlySerAspIleGlySerAspIleGluLeuThrGlnSerProSerS 194

DB 442 CAGCGGAGGTGGCTCTGGCGGGTGGCGGATCTGACATTTGAGCTCACCAGCTCTCCAGCAA 393

QY 194 erLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSerValA 214

DB 382 TCATGCTCATCTCCAGGGAGAGGGGTCCACCTGACCTGCAGTGCAGCTCAAGTATA- 324

QY 214 spSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLysProGlyGlnProProLysL 234

323 -----CGTTACATATATTGTTACCAACAGAAGCCTGGATCTCTCCCCAGAC 278

QY 234 euLeuIleTyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerG 254

DB 277 TCTCATTTATGACATCCACAGTGGCTCTCGGAGTCCCTTTTCGTTCACTGCGAGTG 218

QY 254 lySerGluSerAspPheThrLeuThrIleAspProValGluGluAspAspAlaValT 274

DB 217 GGTCTGGGACCTCTTATTCTCTCAATCAACCGAATGAGGCTGAGGATGCTGCCACTT 158

QY 274 YTYrCysLeuGlnSerMetGluAspProTyrThrPheGlyGlyThrLysLeuGluI 294

DB 157 ATTACTGCCAGAGTGGAGTGGTTATCCGTACACGTTCCGAGGGGACC-AAAGCTGGAGC 99

QY 294 leLYsArg 296

DB 98 TGAACGG 91

RESULT 5

CK629414/c

LOCUS

DEFINITION

CK629414

VERSION

CK629414.1 GI:45753889

KEYWORDS

EST.

SOURCE

Apis mellifera (honey bee)

ORGANISM

Apis mellifera

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.

REFERENCE

1 (bases 1 to 1339)

AUTHORS

Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G., Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F., Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R., Ramos,R.G.P., Reis,L.F.L, Dias Neto,E., Souza,S.J., Simpson,A.J.G., Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M., Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and Silva,W.A. Jr.

TITLE

Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome

JOURNAL

Unpublished (2004)

COMMENT

Contact: Silva Jr, W. A.

Molecular Genetic and Bioinformatics Laboratory

Department of Genetics, FMRP/USP, FUNDHERP

Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 39639300

Fax: +55 16 39639309

Email: wilsonjr@usp.br

This sequence was derived from the FAPESP Genome Program

High quality sequence start: 62

High quality sequence stop: 662.

FEATURES

source

1. .1339

/organism="Apis mellifera"

/mol_type="mRNA"

/strain="Africanized"

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/sex="female, worker"

/dev_stage="adult"

/clone_lib="AA0014"

/note="Organ: whole body"

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Score: 638.00 Matches: 130

Percent Similarity: 74.01% Conservative: 38

Best Local Similarity: 57.27% Mismatches: 45

Query Match: 36.99% Indels: 15

DB: 7 Gaps: 3

US-10-089-278-6 (1-329) x CK629414 (1-1339)

/note="MRP4"; transcript related to the repair of
irradiation-damaged intestinal gland cells treated with
RNA; coding region not determined"

ORIGIN

Alignment Scores:

Pred. No.: 1,066-48 Length: 535
Score: 631.00 Matches: 127
Percent Similarity: 81.82% Conservatives: 17
Best Local Similarity: 72.16% Mismatches: 23
Query Match: 36.58% Indels: 10
DB: 3 Gaps: 2

US-10-089-278-6 (1-329) x AF240170 (1-535)

Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
Db 534 GCGGCCCGCCGCGCCATGCCAGGTGAACCTGCAGCAGTCCAGGACCTCGAGTGGTGAGG 475
Qy 61 ProGlyValSerValLysLeuSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 474 CTGGGGTCTCAGTGAAGATTCTTCGCAAGGTTCCGGCTACACATTCACGTATTATCT 415
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 414 ATGCACCTGGTGAAGATCATGCACAGAGTCTAGAGTGGATTGGAAATTATTAGTACT 355
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 354 TACGATGGTAATACAACTACAAACAGAAAGTTTAAGGGCAAGGCCACTATGACTGTTGAC 295
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 294 AATCTCTCCATTACAGCTATATGAACCTATGCCAGATTGACATCTGATGATTCGCCATC 235
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160
Db 234 TATTACTGTGCAAGAGG---GCTTACTACGGTAGTTTATTACTTTGACTAGTGGGC 178
Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
Db 177 CAAGGGACCAAGTCCAGTCTCCTCAGTGGAGCGGTTCCAGCGGAGGTGGCTCTGGC 118
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 117 GGTGGCGATCGGA-ATCGAGCTCACCAGGGGGCACCAGGATCGGAATCAACCGCGCGC 59
Qy 201 GlnArg-----AlaThrIleSerCysArg 208
Db 58 CGCAGGTGGCGCGGTATCCGGATCCGCTCGGAACCGCGTCCCGC 11

RESULT 9

AF240167 540 bp mRNA linear HTC 30-APR-2001
LOCUS Mus musculus MRP4 mRNA, complete cds.
DEFINITION AF240167
ACCESSION AF240167.1 GI:13877286
VERSION
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE 1 Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 540)
TITLE Tian, F., Zeng, G.Y., Wang, F., Xu, J.R., Ren, D.Q., Guo, Y.H.,
JOURNAL Cui, D., Zeng, G.Y., Hou, Y., and Su, C.Z.
PUBLISHED Mechanism of exogenous nucleic acids and their precursors improving
AUTHORS the repair of intestinal epithelium after gamma-irradiation in mice
TITLE World J. Gastroenterol. 6 (5), 709-717 (2000)
11819679
2 (bases 1 to 540)
REFERENCE Cui, D., Zeng, G., Yan, X., Li, X. and Su, C.
AUTHORS Cloning of mouse genes related to repairing of intestinal
TITLE epithelium of the irradiated mice by treatment with the intestinal

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-089-278-6 (1-329) x AF240167 (1-540)

Qy

Db

Qy

Db

Qy

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Qy

Db

Qy

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Qy

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Qy

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Qy

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Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

RNA of mice of the same strain
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80
(2001)

3 (bases 1 to 540)

Cui, D., Zeng, G., Yan, X., Wang, F., Tian, F., Ren, D., Zhao, T., Li, X.
and Su, C.

Direct Submission

Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of
Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang
Le West Road, Xi'an 710032, China

Location/Qualifiers

1. 540

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/sex="male"

/cell_type="intestinal gland cell"

/note="derived from differential display PCR between
irradiated mice with and without RNA injection"

24. 536

/note="related to the repair of irradiation-damaged
intestinal gland cells treated with RNA"

/codon_start=1

/product="MRP4"

/protein_id="AAK43732.1"

/db_xref="GI:13877287"

/translations="MAQVQLKQKPEVVRPGVSKISKSGYFTFTDSYHMLKNNHA
QSLWIGIIISTYDGNNTNOKFKGATMTVDKSIITAYMELARLITSDSALYYCARGA
YXGPFYFDYWGQGTITVTVSSGGGGGGGGGGSSSSSPGGTKLIRKRAAGAPVP
YDPLEPRAA"

Length: 540
Matches: 127
Conservative: 17
Mismatches: 23
Indels: 10
Gaps: 2

US-10-089-278-6 (1-329) x AF240167 (1-540)

Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60

Db 9 GCGGCCCGCCGCGCCATGCCAGGTGAACCTGCAGCAGTCCAGGACCTCGAGTGGTGAGG 68

Qy 61 ProGlyValSerValLysLeuSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80

Db 69 CTGGGGTCTCAGTGAAGATTCTTCAGAGGTTCCGGCTACACATTCACGTATTATCT 128

Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100

Db 129 ATGCACCTGGTGAAGATCATGCACAGAGTCTAGAGTGGATTGGAAATTATTAGTACT 188

Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120

Db 189 TACGATGGTAATACAACTACAAACAGAAAGTTTAAGGGCAAGGCCACTATGACTGTTGAC 248

Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140

Db 249 AATCTCTCCATTACAGCTATATGAACCTATGCCAGATTGACATCTGATGATTCGCCATC 308

Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160

Db 309 TATTACTGTGCAAGAGG---GCTTACTACGGTAGTTTATTACTTTGACTAGTGGGC 365

Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180

Db 366 CAAGGGACCAAGTCCAGTCTCCTCAGTGGAGCGGTTCCAGCGGAGGTGGCTCTGGC 425

Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200

Db 117 GGTGGCGATCGGA-ATCGAGCTCACCAGGGGGCACCAGGATCGGAATCAACCGCGCGC 59

Qy 201 GlnArg-----AlaThrIleSerCysArg 208

Db 58 CGCAGGTGGCGCGGTATCCGGATCCGCTCGGAACCGCGTCCCGC 11

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Db      426 GGTGGCGGATCGGA-ATCGAGCTCACCAGGGGGCACCAGCTGGAATCAAAACGGCGGC 484
Qy      201 GlnArg-----AlaThrIleSerCysArg 208
Db      485 GCGAGGTGCGCGGTGCGGTATCCGGATCCCGTGGAAACCGGTGCCGC 532

RESULT 10
CK629415/c
LOCUS   CK629415      1419 bp      mRNA      linear      EST 26-MAR-2004
DEFINITION AM1-AA0014-041102-021-H09 AA0014 Apis mellifera cDNA, mRNA
VERSION   CK629415.1
KEYWORDS  EST.
SOURCE    CK629415.1 GI:45753890
ORGANISM  Apis mellifera (honey bee)

REFERENCE
1 (bases 1 to 1419)
Nunes,F.M.F.,Valente,V.,Sousa,J.F.,Cunha,M.A.V.,Pinheiro,D.G.,
Maia,R.M.,Araujo,D.D.,Costa,M.C.R.,Martins,W.K.,Carvalho,A.F.,
Monesi,N.,Nascimento,A.M.,Peixoto,P.M.V.,Silva,M.F.R.,
Ramos,R.G.P.,Reis,L.F.L.,Dias Neto,E.,Souza,S.J.,Simpson,A.J.G.,
Zago,M.A.,Soares,A.E.E.,Bitondi,M.M.G.,Espreafico,E.M.,
Espindola,F.S.,Paco-Larson,M.L.,Simoes,Z.L.P.,Hartfelder,K. and
Silva,W.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br

This sequence was derived from the FAPESP Genome Program
High quality sequence start: 63
High quality sequence stop: 605.

FEATURES
source
1..1419
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stages="adult"
/clone_lib="AA0014"
/note="Organ: whole body"

ORIGIN
Alignment Scores:
Pred. No.:      5,35e-48      Length:      1419
Score:          629.50      Matches:    131
Percent Similarity: 72.32%      Conservative: 31
Best Local Similarity: 58.48%      Mismatches: 50
Query Match:     26.49%      Indels:    15
DB:              7          Gaps:        3

US-10-089-278-6 (1-329) x CK629415 (1-1419)

Qy      75 ThrPheThrAspTyrGlyMetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrp 94
Db      728 ACATTCACAGTATGATATAGACTGGTG-AAGCAGACGCC-TGNACAGGACTTGGATGG 671

Qy      95 IleGlyLeuIleSerThrTyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLys 114
Db      670 ATTGGATG-ATTTTCTCGGAGGAGGANGTACTGAATACATGAGAAGTCAAGGGCAGG 612

Qy      115 AlaThrMetThrValAspLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThr 134
Db      611 CACACACTGGTGTAGACAAGTCTCCAGCACAGCCTATATGGAGCTCACTAGGCTGACA 552

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```

Qy      135 SerGluAspSerAlaIleTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyr 154
Db      551 TCTGAGGACTCTGCTGCTATTCTGTGCTAGAGGGAC-----TACTAT 507

Qy      155 Ala-----LeuAspTyrTrpGlyGlnGlyThrValThrValSerSerGlyGlyGly 172
Db      506 AGCGCGTACTTTGACTTTGTGGGGCAAGGGACCAACGCTCACCCTCTCTCATGTGGAGAC 447

Qy      173 GlySerGlyGlyGlySerGlyGlyGlyGlySerAspIleGluLeuThrGlnSerPro 192
Db      446 GGTTCAGGCGGAGGTGCTCTGCGGTGGCGGATCTGACATTGAGCTCACCCAGTCTCCA 387

Qy      193 SerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCysArgAlaSerGluSer 212
Db      386 GCATCATGCTGCACTCCAGGGGAGAGGGTCCACCATGACCTGCAGTGCAGCTCAAGT 327

Qy      213 ValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLysProGlyGlnProPro 232
Db      326 ATA-----CGTTACATATATTGGTATCCACAGCAAGCGCTGGATCCTCCTCC 282

Qy      233 LysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGly 252
Db      281 AGACTCTCTGATTATGACATCCACAGTGGCTCTCGAGTCCCTTTTCCGCTTCAGTGGC 222

Qy      253 SerGlySerGluSerAspPheThrLeuThrIleAspProValGluGluAspAlaAla 272
Db      221 AGTGGGTCTGGACCTTATTCTTCACCAATCAACGAATGAGGCTGAGGATGCTGCC 162

Qy      273 ValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeu 292
Db      161 ACTTATTACTGCCAGGAGTGGAGTGTATTCCGTACACGTTTCGAGGGGGGACCAAGCTG 102

Qy      293 GluIleLysArg 296
Db      101 GAGCTGAACGC 90

RESULT 11
CK632348
LOCUS   CK632348      823 bp      mRNA      linear      EST 26-MAR-2004
DEFINITION AM0-AM0009-070103-021-H02 AM0009 Apis mellifera cDNA, mRNA
VERSION   CK632348
KEYWORDS  EST.
SOURCE    CK632348.1 GI:45756823
ORGANISM  Apis mellifera (honey bee)

REFERENCE
1 (bases 1 to 823)
Nunes,F.M.F.,Valente,V.,Sousa,J.F.,Cunha,M.A.V.,Pinheiro,D.G.,
Maia,R.M.,Araujo,D.D.,Costa,M.C.R.,Martins,W.K.,Carvalho,A.F.,
Monesi,N.,Nascimento,A.M.,Peixoto,P.M.V.,Silva,M.F.R.,
Ramos,R.G.P.,Reis,L.F.L.,Dias Neto,E.,Souza,S.J.,Simpson,A.J.G.,
Zago,M.A.,Soares,A.E.E.,Bitondi,M.M.G.,Espreafico,E.M.,
Espindola,F.S.,Paco-Larson,M.L.,Simoes,Z.L.P.,Hartfelder,K. and
Silva,W.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br

This sequence was derived from the FAPESP Genome Program
High quality sequence start: 70
High quality sequence stop: 545.

FEATURES
source
1..823

```

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/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stages="Mix of adult, pupal, larval and embryonic."
/clone_lib="AM0009"
/note="Organ: whole body"

ORIGIN
Alignment Scores:
Pred. No.: 9,46e-46 Length: 823
Score: 602.00 Matches: 128
Percent Similarity: 66.01% Conservative: 39
Best Local Similarity: 50.59% Mismatches: 64
Query Match: 34.90% Indels: 22
DB: 7 Gaps: 5

US-10-089-278-6 (1-329) x CK632348 (1-823)
QY 43 GlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArgProGly 62
Db 87 CAGCGGGGATGGCCAGGTAAGCTGCAGAGTCTGGCTACATCTTCACAGTTATGATATAGAC 146
QY 63 ValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSer 82
Db 147 GCTTCAGTGAAGTTGCTCTGCAGAGCTTCTGGCTACATCTTCACAGTTATGATATAGAC 206
QY 83 TrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyr 102
Db 207 TGGGTGAGGAGACGCCCTGACAGCAACTTGGTGGCTTGGATGATTTTCTCTGGAGAG 266
QY 103 GlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSer 122
Db 267 GCGAGTAGTACTCAATCAATGAGAGTTCAAGCGGCGCCACACTGAGTGTAGACAATCC 326
QY 123 SerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyr 142
Db 327 TCAGGACACGCTATATGAGGACTCAGTGGCTGACATCTGAGGACTCTGCTGCTATTTTC 386
QY 143 CysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAla-----LeuAspTyrTrpGly 160
Db 387 TGTGCTAGAGGGGAC-----TACTATAGGCGCTACTTTGACTTGTGGGC 431
QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 180
Db 432 CAAGGGGACCGCTCACCCTCTCTCATGTGAAGCGGTTTCAGCGGAGGCTCTGGC 491
QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAla--ValSerLeuG 200
Db 492 GGTGGCGGATCTGACATGTAGCTCACCAGTCTCCAGCATCATGTCTGCATCTCCAGTG 551
QY 200 lylGlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerP 220
Db 552 GAAGAGGTCACCAATGACCTGAGTGCAGTCAAGCTCAAGTATA-----CGTN 596
QY 220 heMetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIle-----T 237
Db 597 ACATATATTGGTTTCAACAGAGCGTGGATCCTCCCGGAGGCTGATGATGACACATC 656
QY 237 YrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluS 257
Db 657 AAGTGGCCCTGGAGTCTTTCG-----CTCAGTGGCAGGTGGTCTGGACC 701
QY 257 erAspPheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysL 277
Db 702 TCTTATTCTCAAAATCACCAGTGGAGCTGAGATCTGATATATCTGCGGAGTGATGTA 761
QY 277 euGlnSerMetGluAspProTyrThrPheGlyGly 288
Db 762 TCCGACCTTCGGAGGGACCACTGAGCGAAGGGGCG 796

RESULT 12
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AF240172/c
LOCUS AF240172 683 bp mRNA linear HTC 30-APR-2001
DEFINITION Mus musculus MRP9 mRNA, partial cds.
ACCESSION AF240172
VERSION AF240172.1 GI:13877293
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Sukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 683)
Cui,D.X., Zeng,G.Y., Wang,F., Xu,J.R., Ren,D.Q., Guo,Y.H.,
Tian,F.R., Yan,X.J., Hou,Y. and Su,C.Z.
Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice
World J. Gastroenterol. 6 (5), 709-717 (2000)
11819679
2 (bases 1 to 683)
Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
Cloning of mouse genes related to repairing of intestinal
epithelium of the irradiated mice by treatment with the intestinal
RNA of mice of the same strain
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80
(2001)
3 (bases 1 to 683)
Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X.
and Su,C.
Direct Submission
Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of
Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang
Le West Road, Xi'an 710032, China
LOCATION/Qualifiers
1. 683
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/sex="male"
/cell_type="intestinal gland cell"
/notes="derived from differential display PCR between
irradiated mice with and without RNA injection"
<1..352
/notes="related to the repair of irradiation-damaged
intestinal gland cells treated with RNA"
/codon_start=2
/product="MRP9"
/db_xref="GI:13877294"
/db_xref="AAK43734.1"
/translation="LCGTRFQRIRIRHRTTCGRPFQQLGPPSERVRLTLVTEIHC
RIILHRIIVEAIEICPRTPASKPRDPGSLGCSIDEEFGWUSFLLPEVHKTNANII
NTFAGSAGGGPLP"

CDS
(
)

Alignment Scores:
Pred. No.: 1,4e-45 Length: 683
Score: 599.00 Matches: 145
Percent Similarity: 73.59% Conservative: 25
Best Local Similarity: 62.77% Mismatches: 41
Query Match: 34.72% Indels: 23
DB: 3 Gaps: 5

US-10-089-278-6 (1-329) x AF240172 (1-683)
QY 92 LeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSer----- 106
Db 668 TTGAAGTGGATGGC-----TGAATAAACNACCCTCTGAAGTCCCAAG 621
QY 107 TyrAsnGlnArg-PheLysGlyLysAlaThrMetThrValAspLysSer---SerAnth 125
Db 620 TATGCCAAGAGAGTTCAAGGGACGCTTTGCTCTCTTTGAAACCTCTGCAGGCAC 561
QY 125 r-AlaTyrLeuGluLeuAlaArgLeu-ThrSerGluAspSerAlaIleTyrTyrCysAla 144
```

Db 560 TTCATATTTACAGTAAGCAACCTCAAAAAATGAGGACACGCTACGATATTTCTGTATG 501

Qy 145 AtgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThr 164

Db 500 AGATGGGATTACGACGGGGGGTTT-----GCTTACTGGGC-CAAGGGACACG 454

Qy 165 ValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySer 184

Db 453 GTCACCGCTCTCCTCAGGTGGAGC-GGTTCAAGCGGAGGTGGCTCTGGCAGTGGCGGATCG 395

Qy 185 AspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThr 204

Db 394 GACATCGTGTCTACCCAGTCTCCAGCTTCTTGGCTGTGTCTTAGGGCAGAGGGCCACC 335

Qy 205 IleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyr 224

Db 334 ATCTCCTCGCAGACGACGCGAAGGTGTGATAATATTGGCATTAGTTTATGAACCTGGTTC 275

Qy 225 GlnGlnLysProGlyGlnProProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuSer 244

Db 274 CAGCAGAAACAGGACAGCCACCAAACTCTCATCTATCTGTCATCCAAAGCAAGGATCC 215

Qy 245 GlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAsp 264

Db 214 GGGGTCTCTCCAGGTTTACTGGCAGTGGGTCTGGGACAGATTTCAGCCTCAACATATAT 155

Qy 265 ProValGluGluAspAspAlaValTyrTyrCysLeuGlnSerMetGluAspProTyr 284

Db 154 CCTATGAGGAGGATGATCTCGCAGTGTATTTCTGTCCACCAAGTAAAGGAGTTCTCTTAC 95

Qy 285 ThrPheGlyGlyThrLysLeuGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuGly 304

Db 94 ACGTTCGGAGGGGGAGCAAGCTGGAGCTGAACCGGGCGCCGCA-----GGTGC- 45

Qy 305 GlyGlySerGlyGlyGlySerGlyGly 313

Db 44 GCCGGTCCGCTATCCGGATCCGCTGGA 18

RESULT 13

AW988429

LOCUS

DEFINITION

IMAGE:1531021.5' similar to gb:X02484.rnal IG KAPPA CHAIN PRECURSOR

V-IV REGION (HUMAN); gb:M35689 Mouse Ig aberrantly rearranged

kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.

AW988429

AW988429.1 GI:8183581

EST.

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

1 (bases 1 to 407)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:947121

Seq primer: -40RP from Gibco.

Location/Qualifiers

1. 407

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1531021"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/clone_lib="Soares_mammary_gland_NMLMG"

FEATURES

source

Location/Qualifiers

1. 407

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1531021"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/clone_lib="Soares_mammary_gland_NMLMG"

Alignment Scores:

Pred. No.: 8.53e-39 Length: 407

Score: 523.00 Matches: 100

Percent Similarity: 90.52% Conservative: 5

Best Local Similarity: 86.21% Mismatches: 11

Query Match: 30.32% Indels: 0

DB: 2 Gaps: 0

US-10-089-278-6 (1-329) x AW988429 (1-407)

Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200

Db 60 GGTTCACAGGTGACATTGTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTGCTCTAGGG 119

Qy 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220

Db 120 CAGAGGGCCACCATATCTCTGCAGCCAGCGTGAAGTTGATAGTTATGGCAATAGTTTT 179

Qy 221 MetHisTrpTyrGlnGlnLysProGlyGlnProProLysLeuLeuLeuLeuLeuLeuSer 240

Db 180 ATGCACCTGGTACCAGCAGAAACAGGACAGCCACCAAACTCTCATCTATCTGTCATCC 239

Qy 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260

Db 240 AACCTAGAATCTGGGATCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACC 299

Qy 261 LeuThrIleAspProValGluGluAspAlaValTyrTyrCysLeuGlnSerMet 280

Db 300 CTCACCATTAATCTCTGGAGGCTGATGATGTTGCAACCTATTACTGTGACGAAAGTAAT 359

Qy 281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluLeuLeuLeuLeuLeuSer 296

Db 360 GAGGATCCGCTGACGTTCCGTGGAGGACCAACAGCTGGAATCAACCG 407

RESULT 14

BF801321

LOCUS

DEFINITION

MR0-CI0023-241000-102-f09 CI0023 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF801321

VERSION

BF801321.1 GI:12130310

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 565)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Frudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT7T3 vector. Library is normalized. Library "

was constructed by Bento Soares and M. Fatima Bonaldo."

Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-CI0023-241000-102-f09&t3=2000-10-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 501.
Location/Qualifiers
1..565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0023"
/note="Organ: colon; ins; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 2,26e-38 Length: 565
Score: 520.50 Matches: 105
Percent Similarity: 76.36% Conservative: 21
Best Local Similarity: 63.64% Mismatches: 31
Query Match: 30.17% Indels: 8
DB: 2 Gaps: 2

US-10-089-278-6 (1-329) x BF801321 (1-565)

QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValarg 60
DB 35 GCGGCCAGCCGGCCATGTCAGTCAAGTCGACGAGTAAGCACTGAAGTGTAAAG 94
QY 61 ProGlyValSerValLysLeuSerCysLys-GlySerGlyTyrThrPheThrAspTyrGl 80
DB 95 CCTGGGGCTTCAGTGAAGTGTCTCTGCAAGTGTCTGCTACATCTTCAAGTTATGA 154
QY 80 YMetSerTyrValLysGlnSerHisAlaLysSerLeuGluTyrPheGlyLeuLeuSerTh 100
DB 155 TATAGACTGGTGAGGACAGCGCTGACAGGACTTGAAGTGTGATTTGATTTTCC 214
QY 100 rTyrTyrCysAlaArgProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValas 120
DB 215 TCGAGAGGGGAGTACTCAATACAATGAGAAGTTCAAGGGCAGGCCACACTGAGTGTAGA 274
QY 120 pLysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaI 140
DB 275 CAAGTCTCCAGACACACCTATATGGAGCTCACTAGGCTGACATCTGAGGACTCTGCTGT 334
QY 140 eTyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAla-----LeuAspTy 158
DB 335 CTATTTCTGTCTAGAGGGAC-----TACTATAGGGCTACTTTGACTT 379
QY 158 rTyrGlyGlnGlyThrThrValThrValSerSerGlyGlyGlySerGlyGlyGly 178
DB 380 GTGGGGCCAAAGGACACACGTCACGGTCTCTCATGTGGAGGCGGTTCAGCGGAGGTGG 439
QY 178 ySerGlyGlyGlyCysSerAspLeuGluLeuThrGlnSerProSerSerLeuAlaValse 198
DB 440 CTCCTGGCGGTGGGGGATCTGACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCTTC 499
QY 198 rLeuGlyGlnArg 202
DB 500 TCCAGTGGAGAGG 512

RESULT 15
BG965088
LOCUS

738 bp mRNA linear EST 12-JUN-2001

DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
1..738

/organism="Mus musculus"
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4983974"
/lab_host="DHI08 (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN

Alignment Scores:
Pred. No.: 2,23e-37 Length: 738
Score: 511.50 Matches: 107
Percent Similarity: 73.49% Conservative: 15
Best Local Similarity: 64.46% Mismatches: 25
Query Match: 29.65% Indels: 19
DB: 4 Gaps: 3

US-10-089-278-6 (1-329) x BG965088 (1-738)

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QY 25 ValAlaTyrTrpGlyPheGlyThrAlaGluValSerThrAlaArgAlaGlnPro 44
DB 70 GTAGCA-----ACAGCTACAGGT 87
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DB 88 GTACACTCCAGGTCAGCTGCAGCAGTCTGGCCCTGAGCTGGTGGCTGGGGTCTCA 147
QY 65 ValLysLeuSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpVal 84
DB 148 GTGAAGATCTCTGCAAGGGTTCGGCTACACATTCACTGATTATGTATACACTGGGTG 207
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DB 208 AAGCAGAGTCATGCAAGAGTCTAGAGTGGAGTTATTAACTACTTACTATGTAA 267
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mRNA sequence.
BG965088
BG965088.1 GI:14352725
EST.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10989 row: 9 column: 15
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Db	328	ACAGCCTATATGGAACTTGGCCAGATTGACAGCTGAGGATTCTGCCATCTATTACTGTGCA	387
Qy	145	Arg---SerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThr	163
Db	388	AGATTATTGCGGGGAAC-----TATGCTGTGGACTACTGGGGTCAAGGAACC	435
Qy	164	ThrValThrValSerSer	169
Db	436	TCAGTCACCGTCTCTCTCA	453

Search completed: August 23, 2005, 16:40:25
 Job time : 3123 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 14:02:29 ; Search time 198 Seconds

(without alignments)

2718.864 Million cell updates/sec

Title: US-10-089-278-6

Perfect score: 1725

Sequence: 1 MDCLTLNLSAEGKVDQASKI.....GSGGGGSGGSGGSPVQFI 329

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	936.5	54.3	891	2	US-08-894-922A-9
4	935.5	54.2	717	4	US-09-473-653-5
5	935	54.2	996	2	US-08-894-922A-4
6	935	54.2	996	4	US-09-742-693-27
7	918.5	53.2	894	4	US-08-886-814A-1
8	916.5	53.1	797	2	US-08-894-922A-13
9	908	52.6	2019	3	US-09-423-439-31
10	908	52.6	2025	3	US-09-423-439-37
11	894.5	51.9	831	2	US-08-403-853-17
12	881	51.1	1135	4	US-09-203-958A-3

13	880	51.0	807	4	US-09-674-677-4	Sequence 4, Appli
14	878	50.9	864	3	US-09-423-439-47	Sequence 47, Appl
15	853.5	49.5	780	4	US-09-526-738A-3	Sequence 3, Appli
16	844.5	49.0	771	4	US-09-526-738A-1	Sequence 1, Appli
17	842	48.8	732	2	US-08-553-497A-19	Sequence 19, Appl
18	837.5	48.6	717	2	US-08-553-497A-17	Sequence 17, Appl
19	836.5	48.5	1998	3	US-09-423-439-50	Sequence 50, Appl
20	836	48.5	723	4	US-09-581-345-1	Sequence 1, Appli
21	833.5	48.3	1679	2	US-08-661-052-15	Sequence 15, Appl
22	833.5	48.3	1679	3	US-09-188-082-15	Sequence 15, Appl
23	833.5	48.3	1679	3	US-09-364-088-15	Sequence 15, Appl
24	833.5	48.3	1679	3	US-09-102-716-15	Sequence 15, Appl
25	831	48.2	804	3	US-09-485-737B-1	Sequence 1, Appli
26	831	48.2	804	4	US-10-071-485-1	Sequence 1, Appli
27	830.5	48.1	777	4	US-10-092-246-7	Sequence 7, Appli
28	830.5	48.1	777	4	US-10-096-246A-7	Sequence 7, Appli
29	826	47.9	723	1	US-07-988-430-93	Sequence 93, Appl
30	826	47.9	723	1	US-08-425-336-90	Sequence 90, Appl
31	826	47.9	723	1	US-08-488-113B-90	Sequence 90, Appl
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39	825.5	47.9	1176	3	US-09-142-974B-3	Sequence 3, Appli
40	825	47.8	738	2	US-08-553-497A-23	Sequence 23, Appl
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42	824	47.8	779	1	US-08-133-804-3	Sequence 3, Appli
43	824	47.8	779	1	US-08-461-838-3	Sequence 3, Appli
44	824	47.8	779	2	US-08-461-886-3	Sequence 3, Appli
45	823.5	47.7	719	3	US-08-279-772A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-070-408-1
; Sequence 1, Application US/09070408
; Patent No. 6180341
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent L.
; APPLICANT: Georgiou, George
; APPLICANT: Burks, Elizabeth A.
; TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS
; TITLE OF INVENTION: OF PROTEINS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,408
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/045,409
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UT8B:593
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000

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; TELEFAX: 512/447-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1010 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-070-408-1

Alignment Scores:
Pred. No.: 1.03e-77 Length: 1010
Score: 980.00 Matches: 188
Percent Similarity: 86.11% Conservative: 29
Best Local Similarity: 74.60% Mismatches: 31
Query Match: 56.81% Indels: 4
DB: 3 Gaps: 2

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Db 136 GAAGTTCAACTGCAACAGTCTGGTCTGAATTGGTTAAACCTGGCGCTCTGTGGCGCATG 195
Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 196 TCCTGCAAAATCCTCAGGGTACATTTTCCCGCACTTCTACATGAATTGGTTCGCCAGTCT 255
Qy 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 256 CATGGTAAGTCTCTAGACTACATCGGTGATATTTCCCATTTCTGGGGTTACCGGCTAC 315
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 316 AACCAAGATTAAAGTAAGGCCACCTTACTGTCCGACAACTTCTCACTCACTGCTTAC 375
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 376 ATGAGAGCTGGCTTCTTGAACCTCTGAGGACTCCGCGGTACTACTATTCGCGGGTCTCT 435
Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrValThrVal 167
Db 436 GGTAAAC-----AAATGGGCCATGGATTATTTGGGGTTCATGGTGTCTAGCTTACTGTG 486
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySerAspIleGlu 187
Db 487 AGCTCTGGTGGCGGTGCTCGGGCGGTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTAGTA 546
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
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Qy 208 ArgAlaSerGluSer---ValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGln 226
Db 607 CGATCCAGCAAAAGTCTCGTACATCTTAATGGTAATTAATTAATTAATTAATTAATTAAT 666
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Qy 267 GluGluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPhe 286
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Qy 287 GlyGlyGlyThrLysLeuGluIleLysArgAlaAla 298
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RESULT 2
US-08-447-402-6
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; Sequence 6, Application US/08447402
; Patent No. 5866344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Georgiou, George
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION
; TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED
; TITLE OF INVENTION: LIBRARIES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,402
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,543
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/794,731
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UT584\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780
US-08-447-402-6

Alignment Scores:
Pred. No.: 1.1e-77 Length: 780
Score: 978.00 Matches: 187
Percent Similarity: 86.11% Conservative: 30
Best Local Similarity: 74.21% Mismatches: 31
Query Match: 56.70% Indels: 4
DB: 2 Gaps: 2

US-10-089-278-6 (1-329) x US-08-447-402-6 (1-780)
Qy 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
Db 1 GAAGTTCAACTGCAACAGTCTGGTCTGAATTGGTTAAACCTGGCGCTCTGTGGCGCATG 60
Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 61 TCCTGCAAAATCCTCAGGGTACATTTTCCCGCACTTCTACATGAATTGGTTCGCCAGTCT 120
Qy 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
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Qy	168	SerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlySerAspIleGlu	187
Db	352	AGCTCTGTTGGCGGTGGCTCGGGCGGTGGTGGGTGGCGCGGATCAGACATAGTA	411
Qy	188	LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys	207
Db	412	CTGACCCAGTCTCCAGTCTTTTGGCTGTCTCTTAGGCAAAAGGGCCAGCATATCCTGC	471
Qy	208	ArgAlaSerGluSer---ValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGln	226
Db	472	CGATCCAGCCAAAGTCTCGTACATTCTAATGGTAATACTTATCTGAACCTGGTACCAACAG	531
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Qy	247	ProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProVal	266
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Qy	287	GlyGlyGlyThrLysLeuGluIleLysArgAlaAla	298
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RESULT 3

US-08-894-922A-9
; Sequence 9, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOOT, Cornelius P.E.
; APPLICANT: WHITELAM, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468

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 Qy 299 AlaSerGlySerGlyGlyGlyGlySerGlyGlyGly 310
 Db 814 -----GGATCCGGTAGCGGGAACCTCCGGTAAGGGG 843
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 ; Sequence 5, Application US/09473653
 ; Patent No. 6703015
 ; GENERAL INFORMATION:
 ; APPLICANT: Solomon, Beka
 ; APPLICANT: Frenkel, Dan
 ; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
 ; FILE REFERENCE: 00/20785
 ; CURRENT APPLICATION NUMBER: US/09/473,653
 ; CURRENT FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 60/152,417
 ; PRIOR FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 717
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(7)
 ; OTHER INFORMATION: scFv 508F construct
 US-09-473-653-5
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 Pred. No.: 5,68e-74 Length: 717
 Score: 935.50 Matches: 181
 Percent Similarity: 81.85% Conservative: 22
 Best Local Similarity: 72.98% Mismatches: 36
 Query Match: 54.23% Indels: 9
 DB: 4 Gaps: 3
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 Db 1 CAGGTCAAACTGCAGGAGTCAGGGGCTGAGCTGGTGAGGCTGGGGTCTCAGTGAAGATT 60
 Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
 Db 61 TCCTGCAGAGGTTCTGGCTACACATTCACCTGATGATGCTATGCTGGTGAAGCAGAT 120
 Qy 88 HlaAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
 Db 121 CATGCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTACTATGCTGATGCTAGCTAC 180
 Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
 Db 181 AACCAGAAAGTTCAGGCAAGGCCACATGCTGATGACAAATCCCTCAGCAGCCCTAT 240
 Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
 Db 241 ATGGAACCTGCCAGACTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGGG--- 297
 Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrVal 167
 Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCAAAGTACACGGTCCACCGTC 348
 Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySerAspIleGlu 187
 Db 349 TCCTCAGGTGAGGCGGTTTCAGGCGGAGTTGGCTCTGGCGGTGGCGATCGGACATCGAG 408

Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
 Db 409 CTCACCTCAGTCTCCAGCAATCATGCTGCATCTCCAGGGGAGAGGTCCACCATGACCTGC 468
 Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLys 227
 Db 469 AGTGCAGCTCAAGTATA-----AGTTACATGCATCTGGTATCAGCAGAAG 513
 Qy 228 ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyValPro 247
 Db 514 CCAGGCACCTCCCAAGAGATGATTTATGACACATCCAAACTGGCTCTCGAGTCCCT 573
 Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
 Db 574 GCTGCTTCAGTGGCAGTGGTCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAG 633
 Qy 268 GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
 Db 634 GCTGAAGATGCTGCCACTTATTACTGCCATCAGCGGAGTAGTTACCATTCAGGTTCCGA 693
 Qy 288 GlyGlyThrLysLeuGluLys 295
 Db 694 GGGGGGCCAAGCTGGAATAAAA 717
 RESULT 5
 US-08-894-922A-4
 ; Sequence 4, Application US/08894922A
 ; Patent No. 5863765
 ; GENERAL INFORMATION:
 ; APPLICANT: BERRY, Mark John
 ; APPLICANT: DAVIS, Paul James
 ; APPLICANT: VAN DER LOGT, Cornelius P.E.
 ; APPLICANT: WHITELAM, Gary Clark
 ; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: United States
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/894,922A
 ; FILING DATE: 03-SEP-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9504344.4
 ; FILING DATE: 03-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB96/00468
 ; FILING DATE: 01-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kokulis, Paul K.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 60113/341261
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)-861-3503
 ; TELEFAX: (202)-822-0944
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 996 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA
 US-08-894-922A-4

FRAGME

Db 670 TATGGCAATAGTTTATGTCAGTGGTACCAGCAGAAACAGGACAGCCACCCAAACTCCTC 729
QY 236 ILeTyArgAlaSerIenLeuGluSerGlyValProAlaArgPheSerGlySerGlySer 255
Db 730 ATCTATCGTCATCCCAACCTAGAACTGGGATTCCTGCCAGGTTTCAGTGGCAGTGGGTCT 789
QY 256 GluSerAspPheThrLeuThrIleAspProValGluGluAspAlaAlaValTyrTyr 275
Db 790 AGACAGAGACTTCACCTCCACCAATAATCTGTGGAGGCTGATGTTGCAACCTATTAT 849
QY 276 CysLeuGlnSerMetGluAspPro-----TyrThrPheGlyGlyThrLysLeuGlu 293
Db 850 TGTCAACAAGTGTATGATGATTCCTGATACATGTCACGCTTCGGAGGGGGACCAAGCTCGAG 909
QY 294 ILeTyArgAlaAlaAlaSerGlySerGlyGlyGlySerGlyGlyGly 310
Db 910 ATCAACCG-----GGATCCGGTAGCGGGAACCTCCGGTAAGGGG 948

RESULT 7

US-09-486-814A-1
; Sequence 1, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 656259910
; APPLICANT: YAMAMOTO, Hiroko
; APPLICANT: TOHDOH, Naoki
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486, 814A
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
; FEATURE:
; OTHER INFORMATION: Clone: pzeoSVC9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
; OTHER INFORMATION: Identification Method: E
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(111)
; OTHER INFORMATION: Encoding PRE-HV sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (436)..(528)
; OTHER INFORMATION: Encoding a linker sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (838)..(891)
; OTHER INFORMATION: Encoding a TAIL sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(894)
; OTHER INFORMATION: strandedness: double-stranded

US-09-486-814A-1

Alignment Scores:
Pred. No.: 2,42e-72 Length: 894
Score: 918.50 Matches: 182
Percent Similarity: 77.09% Conservative: 30
Best Local Similarity: 66.18% Mismatches: 47
Query Match: 53.25% Indels: 17
DB: 4 Gaps: 4

US-10-089-278-6 (1-329) x US-09-486-814A-1 (1-894)

QY 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyValaGluLeuValArg 60
Db 97 GGGGCCAGCCCGCCATGGCCAGGTGAAGCTGCAGGAGTCAAGACCTGAGCTGGAGAAG 156
QY 61 ProGlyValSerValLysIleSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 157 CTTGGCGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTACTCATTCCTGGCTACAAAC 216
QY 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 217 ATGAAGTGGGTGAAACAGAGCAATGAAAGACCTTGAGTGGATTGGATATATTATTCCT 276
QY 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 277 TCAATATGGTGTACTGGCTACCAACAGAGTTCAGAGCAAGCCACATTCAGTGTAGAC 336
QY 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 337 AAATCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTC 396
QY 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyrGly 160
Db 397 TATTACTGTGCAAGA-----CTGGGACTTGACTACTCGGGC 432
QY 161 GlnGlyThrThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGlySerGly 180
Db 433 CAAGGACCAACCGTCAACCGTCTCTCAGTGAGGCGGTTCAGGCGGAGGTGGCTCTGGC 492
QY 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGly 200
Db 493 GGTGGCGGATCGACATCGAGCTCACTCAGTCTCCAACCAACCATGGCTGCATCTCCCGG 552
QY 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPhe 220
Db 553 GAGAAGATCACTATCACCTGCAGTGCAGCTCAAGTATAAGTTCC-----AATTAC 603
QY 221 MetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSer 240
Db 604 TTGCATTGTTATCAGCAGAGCCAGGATTCCTCCCTAAACTCTGATTATAGGACATCC 663
QY 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 664 AATCTGGCTTCTGGAATCCAGCTCGCTCAGTGCGAGTGGGTCTGGGACCTCTTACTCT 723
QY 261 LeuThrIleAspProValGluGluAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
Db 724 CTCACAAATTGGCACCATGGAGGCTGAAGATGTTGCCACTTACTTACTGCCAGCGGTAGT 783
QY 281 GluAspPro-----TyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAla 298
Db 784 AGTATACCAACGATATTCAGTTCTGGTGTGGGACAAAGTTGGAATATAAACCGCGGCC 843
QY 299 AlaSerGlySerGlyGlyGlySerGlyGlySerGlyGlyGly 313
Db 844 GCA-----GGTGC-GCCGTCGCTATCCGGATCCGCTGGA 878

RESULT 8

US-08-894-922A-13
; Sequence 13, Application US/08894922A
; Patent No. 5863765
; GENERAL INFORMATION:
; APPLICANT: BERRY, Mark John
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelius P.E.
; APPLICANT: WHITEHAM, Gary Clark
; TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.

```
;
; COUNTRY: United States
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,922A
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9504344.4
; FILING DATE: 03-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00468
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul K.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 60113/241261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-861-3503
; TELEFAX: (202)-822-0944
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-08-894-922A-13

Alignment Scores:
Pred. No.: 3,13e-72 Length: 797
Score: 916.50 Matches: 186
Percent Similarity: 76.87% Conservative: 20
Best Local Similarity: 69.40% Mismatches: 41
Query Match: 53.13% Indels: 21
DB: 2 Gaps: 4

US-10-089-278-6 (1-329) x US-08-894-922A-13 (1-797)

QY 45 AlaMetAlaGluValLysLeuGlnSerGlyAlaGluValArgProGlyValSer 64
Db 3 GCTTACCTACAGTGGCAGCTGCGAGCAGTCTGGGGCTGAAGTGGAGCGCTTCT 62
QY 65 ValLysLeuSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyrVal 84
Db 63 GTGAGCTGTCTGCAAGGCTTCGACTACACCTTACAGTATTATGGATGCACTGGTG 122
QY 85 LysGlnSerHisAlaLysSerLeuGluTyrPileGlyLeuLeuSerThrTyrTyrGlyAsp 104
Db 123 AAGCAGAGCGCTCGACAAAGCGCTTGGTGGATTGGAGAGATTAACTTACCAACGGTCT 182
QY 105 ProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsn 124
Db 183 ACTTATTACAAATGAGAAGTTCAGAGCAGCGCCACACTGCTAGTACAAATCTCCAGT 242
QY 125 ThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAla 144
Db 243 ACAGCTACATGACGCTCAGCAGCGCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCA 302
QY 145 ArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThr 164
Db 303 AGACGGTATGGTAAC-----TCCTTTGACTACTGGGGCCCAAGGACCAACG 347
QY 165 ValThrValSerSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer 184
Db 348 GTACCGGTCTCC-----TCACGAATGGATAAAGG 377
QY 185 AspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThr 204
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;
; GACATCGAGCTCACCAGTCTCCAGATTCTTTGGCTGTCTCTAGGGCAGAGGGCCACC 437
;
; ILeSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyr 224
;
; ATATCTCTGCAGAGCCAGTGAAGTGTGTATGATGTTATGCAATAGTTTTATGTCAGTGGTAC 497
;
; GlnGlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSer 244
;
; CAGCAGAAACAGACAGCCAGCCCAAACTCTCTATCTATCTGTCATCAACCTAGAATCT 557
;
; GlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAsp 264
;
; GCGATCTCTGCCAGTTCAGTGGCACTGGTCTAGGACAGACTTCACCTCACCATTAAAT 617
;
; ProValGluGluAspAlaIleValTyrCysLeuGlnSerMetGluAspPro--- 283
;
; CTTGTGGAGGCTGATGATGTTGCAACCTATTATTGTCAAAAGTGTATGATTCCTGATC 677
;
; ---TyrThrPheGlyGlyThrLysLeuGluIleLysArgAlaAlaSerGlySer 302
;
; ATGTACACGTTCCGAGGGGGGCAAGCTCGAGATCAACGG-----GGATCC 725
;
; GlyGlyGlyGlySerGlyGly 310
;
; GGTAGCGGAACCTCCGTAAGGG 749
;
RESULT 9
US-09-423-439-31
; Sequence 31, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NOV-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2019 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-423-439-31

Alignment Scores:
Pred. No.: 6.01e-71 Length: 2019
Score: 908.00 Matches: 179
Percent Similarity: 76.70% Conservative: 35
Best Local Similarity: 64.16% Mismatches: 45
Query Match: 52.64% Indels: 20
DB: 3 Gaps: 5
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[illegible]

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Db 595 CAGAGACAGGCGAGTCTCTAAACTGCTGATCTATTGGGCATCCATAGACATCTGGG 654
Qy 246 ValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspPro 265
Db 655 GTCCCTGATCGCTTCACAGGCGAGTGGATCTGGGACAGATTCTCACTCTCAGCATCAGCAGT 714
Qy 266 ValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyr--- 284
Db 715 GTGAGCGCTGAAGACCTGGCAATTATTACTGCAAGCAATCT-----TATACT 762
Qy 285 -----ThrPheGlyGlyThrLysLeuGluLeuLysArgAlaAlaAspSerGlySer 302
Db 763 CTTCGGACGTTCCGTGGAGGACCAAGCTCGAGATCAACGG----- 804
Qy 303 GlyGlyGlyGlySerGlyGlyGlySerGlySerGlyGlyGlySerGlyGlyGlySer 321
Db 805 -----GGCGGTGGTGGCTCCGGAGGTGGCGGTAGCGGTGGCGGGGTTC 849

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RESULT 11

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; US-08-403-853-17
; Sequence 17, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALEY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..819

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..819
; US-08-403-853-17

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Alignment Scores:
Pred. No.: 2,93e-70 Length: 831
Score: 894.50 Matches: 171
Percent Similarity: 79.61% Conservative: 32
Best Local Similarity: 67.06% Mismatches: 47
Query Match: 51.86% Indels: 5
DB: 2 Gaps: 2

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US-10-089-278-6 (1-329) x US-08-403-853-17 (1-831)

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Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArg 60
Db 46 GCTGCCCAACAGCAGATGGCGAGGTGCAGCTGCAGCAGTCTGGGGTGAACATGAGTGAAG 105
Qy 61 ProGlyValSerValLysLysSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 106 CCTGGGGCCCTCAGTGAGGATGCTCTCAAGGCTTCTGGCTACACATTTACCAATTACAAAC 165
Qy 81 MetSerTyrValLysGlnSerHisAlaLysSerLeuGluTyrPheGlyLeuLysSerThr 100
Db 166 ATGTACTGGGTAAACAGTCACCTGGACAGGGCTGGAGTGGATTTGGAAATTTTATCCA 225
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 GGAATGGTGATACTTCTTACATCAGAGTTCAAAGACAAGCCACATTCGCTGCTGAC 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AAATCCTCCAACACAGCTACATGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTC 345
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrTyrTyrTyrTyrTyrTyrTyr 160
Db 346 TATTACTGTGCAAGATCGGGGGCTCTCTATAGATAGACGAGGCTTTGACTCTGGGGC 405
Qy 161 GlnGlyThrThrValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGly 180
Db 406 CAAGGACCAACCGGTCCCGTC---TCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 462
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerSerLeuAlaValSerLeuGly 200
Db 463 GGTGGTGGTTCGGATATCGAGCTCACACAGACTACATCTCCCTCTGCTGCTCTCTGCGGA 522
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerValAspSerValAspSerTyrGlyAspSerPhe 220
Db 523 GACAGAGTCACCATCAGTTGACGGGCAAGTCAGGACATTAAGTAATAT----- 570
Qy 221 MetHisTyrTyrGlnGlnLysProGlyGlnProLysLeuLeuLeuIleTyrArgAlaSer 240
Db 571 TTAACCTGGTATCAACAGAAATCCAGATGGAACCTGTTAACTCCTGATCTACTACACATCA 630
Qy 241 AsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThr 260
Db 631 AATTTACACTCAGAAAGTCCCATCCAGTTCAGTGGCAGTGGGTCTCGAACACAGATTATCT 690
Qy 261 LeuThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMet 280
Db 691 CTCACCATTAGCAACCTGGAAACAAGAAATATTGCCACTTACTTTTGGCCAACAGGATTTT 750
Qy 281 GluAspProTyrThrPheGlyGlyGlyThrLysLeuGluLeuLys 295
Db 751 ACGCTTCGGTTCACGTTCCGAGGGGGGACCAAGCTCGAGATAAGA 795

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RESULT 12

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; US-09-203-958A-3
; Sequence 3, Application US/09203958A
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELER, Tibor

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Qy 86 GlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspPro 105
Db 123 CAGAGTCATGCCAAGAGCTAGAGTGGATTGGACTTATTAGTAATTCCTTTGGTAATACA 182
Qy 106 SerTyrAsnGlnArgPheLysGlyAlaThrMetThrValAspLysSerSerAsnThr 125
Db 183 AACTACACCAAGAGTTTGGAGCCCAAGCCACATGACTGTAGACAAATCCTCCACACACA 242
Qy 126 AlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArg 145
Db 243 GGCTATTGTGAACCTGGCAGATTGACATCTGAGGATTCTGCCATCTATTACTGTGCAAGA 302
Qy 146 SerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrVal 165
Db 303 GTG-----ATCGACTGGTCCCTTCGATGCTCGGGCCCAAGGACCAACCGGTC 347
Qy 166 ThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAsp 185
Db 348 ACCGTCTCTCAGGTGGAGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGAC 407
Qy 186 IleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIle 205
Db 408 ATTGTGTGTCACCAATCTCCAGCAATCATGTTGCACTCTCCAGGGGAGAGGTCCACCATG 467
Qy 206 SerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyrGln 225
Db 468 ACCGTGAGTCCCAATCAGGTGTC-----AGGTACGTGGCACTGGTACCAA 512
Qy 226 GlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly 245
Db 513 CAGAAGTCAGGCACCTCCCCCAAGATGGATTATGACACATCCAACTGGCTCTGGA 572
Qy 246 ValProAlaArgPheSerGlySerGlySerGlySerGlySerPheThrLeuThrIleAspPro 265
Db 573 GTCCCTCTCGCTTCACTGGCAGTGGGTCTGGGACCTCTCACTCTCTCACAATCAGCAGC 632
Qy 266 ValGluGluAspAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThr 285
Db 633 TTGAGGCTCAAGATGCTGCACCTATTACTGCGACACTGGGAGTAGTAACCTCCACAG 692
Qy 286 PheGlyGlyThrLysLeuGluIleLysArgAlaAla 299
Db 693 TTCGGTCTGGACCAAGCTGGAAATAAACGGGCGCGCA 734

RESULT 14
US-09-423-439-47
; Sequence 47, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09423.439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
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; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-423-439-47

Alignment Scores:
Pred. No.: 8 87e-69 Length: 864
Score: 878.00 Matches: 172
Percent Similarity: 79.31% Conservative: 35
Best Local Similarity: 65.90% Mismatches: 44
Query Match: 50.90% Indels: 10
DB: 3 Gaps: 4

US-10-089-278-6 (1-329) x US-09-423-439-47 (1-864)
Qy 41 AlaAlaGlnProAlaMetAlaGluValLysLeuGlnGlnSerGlyAlaGluLeuValArg 60
Db 46 GCTGCCCAACCAAGCCATGGCCAGGTCCAACTGCAGCAGCCTGGGGCTGAACGTGTAAG 105
Qy 61 ProGlyValSerValLysLysSerCysLysGlySerGlyTyrThrPheThrAspTyrGly 80
Db 106 CTTGGGGCTTCACTGAGCCTGCTCTGCAAGGCTTCTGGCTACACCTTCCACCGGTACTGG 165
Qy 81 MetSerTrpValLysGlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThr 100
Db 166 ATACACTGGTGAAGCAGAGCGCTTGCAGAGCGCTTGGAGTGGAGGTTAATCTCT 225
Qy 101 TyrTyrGlyAspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAsp 120
Db 226 AGTACCGGTCTGCTGACTACATGAGAGTTTCAAGAACCAAGGCCACACTGACTGTAGAC 285
Qy 121 LysSerSerAsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIle 140
Db 286 AATCTCTCACCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTC 345
Qy 141 TyrTyrCysAlaArgSerAspGlyAsnTyrGlyTyrTyrAlaLeuAspTyrTrpGly 160
Db 346 TATTACTGTGCAAGA---GAGAGGGCTATGTTACAGATGCTATGGACTACTGGGC 402
Qy 161 GlnGlyThrValThrValSerSerGlyGlyGlySerGlyGlyGlyGlyGlySerGly 180
Db 403 CAAGGGACCAACCGTCACTCTCCTCAGGTGGCGGTGGCTCGGGCGGTGGTGGGT 462
Qy 181 GlyGlyGlySerAspIleGluLeuThrGlnSerProSerSerSerLeuAlaValSerLeuGly 200
Db 463 GCGCGCGGATCTGACATTGAGCTCTCACAGTCTCCATCTCTCCCTGCTGTGTGAGCAGGA 522
Qy 201 GlnArgAlaThrIleSerCysArgAlaSerGluSerVal-----AspSerTyrGlyAsp 218
Db 523 GAGAAGTCACCATGAGCTGCAATCCAGTCAGAGTCTCTCTCAACAGTAGAACCCGNAAG 582
Qy 219 SerPheMetHisTrpTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArg 238
Db 583 AACTACTTGGCTTGGTACCAGCAGACAGACAGGCGGAGTCTCTCTAACTGCTGATCTATTGG 642
Qy 239 AlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAsp 258
Db 643 GCATCCACTAGGACATCTGGGGTCCCTGATCGCTTTCACAGGAGTGGATCTGGGACAGAT 702
Qy 259 PheThrLeuThrIleAspProValGluAlaAspAlaValTyrTyrCysLeuGln 278
Db 703 TTCACCTCTCACCATCAGAGTGTGAGGCGGTGAAGACCTGCAATTTATTACTCAAGACAA 762
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RESULT 15

US-09-526-738A-3
; Sequence 3, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526, 738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Humanus
US-09-526-738A-3

Alignment Scores:
Pred. No.: 1,14e-66 Length: 780
Score: 853.50 Matches: 171
Percent Similarity: 75.00% Conservatives: 30
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Query Match: 49.48% Indels: 15
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US-10-089-278-6 (1-329) x US-09-526-738A-3 (1-780)

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QY 86 GlnSerHisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspPro 105
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QY 106 SerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThr 125
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QY 166 ThrValSerSerGlyGlyGlySerGlyGlySerGlyGlySerGlyGlySerAsp 185
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QY 186 IleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIle 205
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QY 206 SerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGln 225
Db 463 ACCTGCAGTGCAGCTCAAGTGTA-----AATTACATGCACCTGGTCCAG 507
QY 226 GlnLysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGly 245
Db 508 CAGAAGCCAGCGCACTTCTCCCAAACTCTGGATTCTTAGCACATCCCAACCTGGCTTCTGGA 567

QY 246 ValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspPro 265
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QY 306 GlySerGlyGlySerGlyGly 313
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Job time : 206 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2005, 14:42:34 ; Search time 8176 Seconds
(without alignments)
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Delop 6.0 , Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	978	56.7	780	10 US-09-782-671B-1	Sequence 1, Appli
3	978	56.7	780	11 US-09-813-444-1	Sequence 1, Appli
4	976.5	56.6	1817	11 US-10-489-626-4	Sequence 4, Appli
5	948.5	55.0	1906	21 US-10-491-653-25	Sequence 25, Appli
6	947.5	54.9	756	16 US-10-169-351-68	Sequence 68, Appli
7	935.5	54.2	717	9 US-09-808-037-5	Sequence 5, Appli
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15	932.5	54.1	744	21 US-10-610-452-13	Sequence 13, Appli
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17	923	53.5	879	9 US-09-978-752-22	Sequence 22, Appli
18	918	53.2	2952	19 US-10-296-085A-30	Sequence 30, Appli
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20	917.5	53.2	1605	18 US-10-221-131-32	Sequence 32, Appli
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ALIGNMENTS

RESULT 1
US-09-782-672-1
; Sequence 1, Application US/09782672
; Publication No. US20030036092A1
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; Georgiou, George
; Chen, Gang
; Olsen, Mark J.
; Daugherty, Patrick S.
; TITLE OF INVENTION: Directed Evolution of Enzymes and
; Antibodies
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433


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QY 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
DB 121 CATGGTAAGTCTCTAGACTACATCGGTACATTTCCCATCTCTGGGGTACCGGCTAC 180
QY 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
DB 181 AACCAAGTTTAAAGTAAGGCGCACCTTACTGTGCACAAATCTTCTCAACTGCTTAC 240
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QY 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrValThrVal 167
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; Sequence 1, Application US/09813444
; Publication No. US20040072740A1
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
;             Georgiou, George
;             Chen, Gang
;             Olsen, Mark J.
;             Daugherty, Patrick S.
; TITLE OF INVENTION: Directed Evolution of Enzymes and
;                   Antibodies
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,444
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSB620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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US-10-089-278-6 (1-329) x US-09-813-444-1 (1-780)
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RESULT 4
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; Sequence 4, Application US/10489626
; Publication No. US20050079170A1
; GENERAL INFORMATION:
; APPLICANT: LEGALL, Fabrice
; APPLICANT: KIPRIYANOV, Sergey
; APPLICANT: REUSCH, Uwe
; APPLICANT: MOLDENHAUER, Gerhard
; APPLICANT: LITTLE, Melvyn
; TITLE OF INVENTION: DIMERIC AND MULTIMERIC ANTIGEN BINDING STRUCTURE
; FILE REFERENCE: 03528.0142.PCUS00
; CURRENT APPLICATION NUMBER: US/10/489, 626
; CURRENT FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1817
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid
US-10-489-626-4

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Qy 237 TyrArgAlaSerAsnLeuGluSerGlyValProAlaArgPheSerGlySerGlySerGlu 256
Db 768 TATCATGCATCAATCTAGTTTCTGGATCCACACCCAGCTTTAGTGGCAGTGGGTCTGGG 827
Qy 257 SerAspPheThrLeuThrIleAspProValGluGluAspAlaValTyrTyrCys 276
Db 828 ACAGACTTCACCTCAACATCCATCCTGTGGAGAGGTGGTGCCTGCAACCTTACTGT 887
Qy 277 LeuGlnSerMetGluAspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArg 296
Db 888 CAGCAAGTACTGAGGATCCGTGGAGCTTCGGTGGAGGCCACCAAGCTGGAATCAACCG 947
Qy 297 AlaAlaAlaSerGlySerGlyGlyGlySer---GlyGlyGlySerGlyGlyGlyGly 315
Db 948 GCTGATGCTGCGCGCGCTGGTGGTGGTCTTCTGGCGCGCGTGGTAGCGGTGGTGGCGCG 1007
Qy 316 SerGlyGlyGlyGlySer 321
Db 1008 TCCGGTGGTGGTGGTAGC 1025

RESULT 5
US-10-491-653-25
; Sequence 25, Application US/10491653
; Publication No. US20050059082A1
; GENERAL INFORMATION:
; APPLICANT: Breitling, Frank
; APPLICANT: Moldenhauer, Gerhard
; APPLICANT: Poustka, Annemarie
; APPLICANT: Kuhlwein, Thorsten
; APPLICANT: Luttgau, Sandra
; TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins
; FILE REFERENCE: 4121-162
; CURRENT APPLICATION NUMBER: US/10/491,653
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: EP 01123596.7
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP02/10852
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-491-653-25

Alignment Scores:
Pred. No.: 1,33e-78 Length: 1906
Score: 948.50 Matches: 186
Percent Similarity: 81.40% Conservative: 24
Best Local Similarity: 72.09% Mismatches: 39
Query Match: 54.99% Indels: 2
DB: 21 Gaps: 2

US-10-089-278-6 (1-329) x US-10-491-653-25 (1-1906)
Qy 44 ProAlaMetAlaGluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyVal 63
```

Db 908 CCACCGTCCCAAGTTTCAGCTGCAGCAGTCTGGGCTGAACCTGTTGAGGCTGGGGTC 967
Qy 64 SerVallylsleSerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyr 83
Db 968 TCAGTGAAGATTTCTGCAAGGGTTCTGGCTACAAATTCATGATATGCTAGCAGCTGG 1027
Qy 84 ValLysGlnSerHisAlaLysSerLeuGluTyrPheGlyLeuIleSerThrTyrGly 103
Db 1028 GTGMAACAGAGTCATGCAAGAGTCTAGAGTGGATTGGAGTTATTAGTACTTATATGGT 1087
Qy 104 AspProSerTyrAsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSer 123
Db 1088 GATACTACTTATAACCAAGAGTTCAAGGGCAAGGCCACAATGACTGTCCGACAAATCCTCC 1147
Qy 124 AsnThrAlaTyrLeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCys 143
Db 1148 AGCACAGCCCTATATGGAATTCACAGACTCCACATCTGATGATTTCTGCATCTATTATGT 1207
Qy 144 AlaArgSerAspGlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyrGlyGlnGlyThr 163
Db 1208 GCC-----CTGTTAGGCCCTTTCTGCTTACTGGGGCCAAAGGACC 1246
Qy 164 ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGly 183
Db 1247 ACGGTACCGTCTCTCAGGTGAGGGCGGTTTCAAGCGAGGTGGCTCTGGCGGTGGCGGA 1306
Qy 184 SerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAla 203
Db 1307 TCGGACATCGAGTCACTCAGTCTCCATCTCCCTGAGTGTGTGAGCAGGAGAGAAGGTC 1366
Qy 204 ThrIleSerCysArgAlaSerGluSerValAspSerTyrGly-----AspSerPheMet 221
Db 1367 ACTATGAGCTGCAAGTCCAGTCAAGTCTGTTAAACAGTGGAAATCAAATAACGACTTG 1426
Qy 222 HisTyrTyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsn 241
Db 1427 GCCTGGTACCAGCAGAAACAGGGCAACGTCCTAAACTGTGATCTACGGGGCATCCACT 1486
Qy 242 LeuGluSerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeu 261
Db 1487 AGGGAATCTGGGGTCCCTGATCTGCTCACAGCGAGTGGATCTGGAACCGGATTTCACTCT 1546
Qy 262 ThrIleAspProValGluGluAspAspAlaAlaValTyrTyrCysLeuGlnSerMetGlu 281
Db 1547 ACCATCAGCAGTGTGAGGCTGAAGACCTGGCAGTTTATTACTGTGAGATGATCATAGT 1606
Qy 282 AspProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAla 299
Db 1607 TATCCGTTAACGTTCCGTTGCTGCGCACCAAGCTGGAATCAAACGGGGCGCT 1660

RESULT 6

US-10-169-351-68
; Sequence 68, Application US/10169351
; Publication No. US20030157090A1
; GENERAL INFORMATION:
; APPLICANT: BENVENUTO, EUGENIO
; APPLICANT: FRANCONI, ROSELLA
; APPLICANT: DESIDERIO, ANGIOLA
; APPLICANT: TAVLADORAKI, PARASKEVI
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
; TITLE OF INVENTION: WHICH INCLUDE THEM
; FILE REFERENCE: 4161-4
; CURRENT APPLICATION NUMBER: US/10/169,351
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/IT00/00554
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: IT RM99A000803
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 756
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-169-351-68

Alignment Scores:

Pred. No.: 5.8e-79 Length: 756
Score: 947.50 Matches: 180
Percent Similarity: 82.61% Conservative: 29
Best Local Similarity: 71.15% Mismatches: 39
Query Match: 54.93% Indels: 5
DB: 16 Gaps: 2

US-10-089-278-6 (1-329) x US-10-169-351-68 (1-756)

Qy 48 GluValLysLeuGlnGlnSerGlyAlaGluLeuValArgProGlyValSerValIle 67
Db 1 CAGGTGCAGCTGCAGGAGTCTGGGGGAGACTTAGTCAGGCTCGAGGGTCCCTGAAACTC 60
Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyrValLysGlnSer 87
Db 61 TCCTGTGCAGCTCTCGGATTCACCTTTCAGTAGCTATGGCATGTCTGGGTTCGCCAGACT 120
Qy 88 HisAlaLysSerLeuGluTyrPheGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 121 CCAGACAAGAGGTGGAGTTGGTCCCAACCAITTAAGTAATGGTGTAGCACCTTTTAT 180
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 181 CCAGACAGTGTGAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 241 CTGCAATGAGCAGTCTGAAGTCTGAGGACACAGCCATGATTACTGTGCAAGAAGA-- 297
Qy 148 GlyAsnTyrGlyTyrTyrTyrAla-----LeuAspTyrTyrGlyGlnGlyThr 163
Db 298 AGGAATATCCCTTATTACTACGGTAGTAGAGGCTACTTTGACTACTTGGGGCCAAAGGACC 357
Qy 164 ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 183
Db 358 ACGGTACCGTCTCTCAGGTGGAGCGGTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGA 417
Qy 184 SerAspIleGluLeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAla 203
Db 418 TCGGACATCGAGTCACTCAGTCTCCAGCTTCTTGGCTGTGTCTCTAGGGCAGAGGGCC 477
Qy 204 ThrIleSerCysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyr 223
Db 478 ACCATATCTGCAGAGCCAGTGAAGTGTGATAGTTATGGCAATAGTTTTATGCACCTGG 537
Qy 224 TyrGlnGlnLysProGlyGlnProLysLeuLeuIleTyrArgAlaSerAsnLeuGlu 243
Db 538 TACCAGCAAGAACAGGACAGCCACCCAACTCCTCATCTATCGTCATTAATCTAGAA 597
Qy 244 SerGlyValProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIle 263
Db 598 TCTGGGATCCCTGCCAGGTTCAGTGGCAGTGGTCTTAGGACAGACTTACCCTCACCATT 657
Qy 264 AspProValGluGluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspPro 283
Db 658 AATCTGTGGAGGCTGATGATGTTCACCTATTACTGTGAGCAAAAGTAAATGAGGATCCG 717
Qy 284 TyrThrPheGlyGlyGlyThrLysLeuGluIleLysArg 296
Db 718 TGGACGTTCCGTTGGAGGCCAACCAAGCTCGAGATCAAAACGG 756

RESULT 7

US-09-808-037-5
; Sequence 5, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:

Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyrGlyGlnGlyThrThrValThrVal 167
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCCAAGTGACCAAGTCCCGTC 348
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleGlu 187
Db 349 TCCTCAGGTGGAGCGGTTCAGGCGGAGTTGGCTCTGGCGGTGGCGGATCGGACATCGAG 408
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 409 CTCACTCAGTCTCAGCAATCATGCTGCATCTCCAGGGGGAAGGTCCACATGACCTGC 468
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLys 227
Db 469 AGTCCAGCTCAAGTATA-----AGTTACATGCATGGTATCAGCAGAG 513
Qy 228 ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGlySerGlyValPro 247
Db 514 CCAGGCACCTCCCCAAAAGATGATTTATGACACATCCAAACTCTGCGGTCTTGGAGTCCCT 573
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db 574 GCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTATTCTCTCAAAATCAGCAGATGGAG 633
Qy 268 GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 634 GCTGAAGATGCTGCCACTTATTACTGCATCAGCGGAGTAGTTACCACTTCCAGCTTCGGA 693
Qy 288 GlyGlyThrLysLeuGluIleLys 295
Db 694 GGGGGGGCCCAAGCTGGAATAAAAA 717

RESULT 9

US-10-384-788-5
; Sequence 5, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON-2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162,889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2

SEQ ID NO 5

LENGTH: 717

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(717)

US-10-384-788-5

Alignment Scores:

Pred. No.: 7,19e-78 Length: 717

Score: 935.50 Matches: 181

Percent Similarity: 81.85% Conservative: 22
Best Local Similarity: 72.98% Mismatches: 36
Query Match: 54.23% Indels: 9
DB: 17 Gaps: 3

US-10-089-278-6 (1-329) x US-10-384-788-5 (1-717)

Qy 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValIleVal 67
Db 1 CAGGTCAAACTGCAGGAGTCAGGGCTGAGCTGGTGGAGGCTGGGGTCTCAGTGAAGATT 60
Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyrValGlnSer 87
Db 61 TCCTGCAAGGTTCTGGCTACACATTCACATGATTTATGCTATGCACTGGTGAAGCAGAGT 120
Qy 88 HisAlaLysSerLeuGluTyrIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 121 CATGCCAAAGATCTAGAGTGGATTGGAGTTATTAGTACTTACTATGCTGATGCTAGCTAC 180
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerAsnThrAlaTyr 127
Db 181 AACAGAAAGTTCAAGGGCAAGGCCAACATGACTGTAGACAAATCCTCCAGCAGCCTAT 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 241 ATGGAATTCGCCAGCTGACATCTGAGGATCTGCCATCTATTACTGTGCAAGAGGG--- 297
Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTyrGlyGlnGlyThrThrValThrVal 167
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCCAAGTGACCAAGTCCCGTC 348
Qy 168 SerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleGlu 187
Db 349 TCCTCAGGTGGAGCGGTTCAGGCGGAGTTGGCTCTGGCGGTGGCGGATCGGACATCGAG 408
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys 207
Db 409 CTCACTCAGTCTCAGCAATCATGCTGCATCTCCAGGGGGAAGGTCCACATGACCTGC 468
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTyrTyrGlnGlnLys 227
Db 469 AGTCCAGCTCAAGTATA-----AGTTACATGCATGGTATCAGCAGAG 513
Qy 228 ProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGlySerGlyValPro 247
Db 514 CCAGGCACCTCCCCAAAAGATGATTTATGACACATCCAAACTCTGCGGTCTTGGAGTCCCT 573
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db 574 GCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTATTCTCTCAAAATCAGCAGATGGAG 633
Qy 268 GluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 634 GCTGAAGATGCTGCCACTTATTACTGCATCAGCGGAGTAGTTACCACTTCCAGCTTCGGA 693
Qy 288 GlyGlyThrLysLeuGluIleLys 295
Db 694 GGGGGGGCCCAAGCTGGAATAAAAA 717

RESULT 10

US-10-618-856-5

; Sequence 5, Application US/10618856

; Publication No. US20040052766A1

; GENERAL INFORMATION:

; APPLICANT: SOLOMON, Beka

; APPLICANT: FRENKEL, Dan

; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY

; FILE REFERENCE: SOLOMON-2A

; CURRENT APPLICATION NUMBER: US/10/618,856

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: US/09/473,653A

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: US 60/152,417

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; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-618-856-5

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Alignment Scores:	
Pred. No.:	7,19e-78
Score:	935.50
Length:	717
Percent Similarity:	81.85%
Matches:	181
Best Local Similarity:	72.98%
Conservative:	22
Mismatches:	36
Query Match:	54.23%
Indels:	9
DB:	18
Gaps:	3

US-10-089-278-6 (1-329) x US-10-618-856-5 (1-717)

	Qy	48	GluValLysLeuGlnClnSerGlyAlaGlnIleuValArgProGlylValSerValLysIle67
			:::::
	Db	1	CAGGTCAAACTCGCAGAGTCAGGGCTCGAGCTGGTGAGCCCTGGGGTCTCAGTCAAGATT60
			:::::
	Qy	68	SerCyLeLysGlySerGlyTyrrThrPheThrAspTyrrGlyMetSerTrpValLysGlnSer87
			:::::
	Db	61	TCTCTGAACGGTTCTGGCTACACATTCACTGATTATGCTATGCATCTGGGTGAAGCAGAGT120
			:::::
	Qy	88	HisAlaLysSerLeuGlnTrpIleGlyLeuIleSerThrrTyrrTyrrGlyAspProSerTyr107
			:::::
	Db	121	CATGCCAAGAGCTAGAGTGGATTGGAGTATTAGTACTTACTATGGTGATGCTAGCTAC180
			:::::
	Qy	108	AsnGlnArpPheLysGlyLysAlaThrMetThrValAspLysSerSerAsenThrAlaTyr127
			:::::
	Db	181	AACCAGAAGTTCAAGGGCAAGCCACAATGACTGTAGACAAATCCTCCAGCACAGCCTAT240
			:::::
	Qy	128	LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrrTyrrCyLeAlaAArgSerAsp147
			:::::
	Db	241	ATGGAACTTGCACAGACTGACATCTCAGAGATTCTGCACATCTATTACTGTGCAAGAGGG---297
			:::::
	Qy	148	GlyAsnTyrrGlyTyrrTyrrAlaLeuAspTyrrTrpGlyGlnGlyThrrThrrValThrrVal167
			:::::
	Db	298	GCTACTATGCTCTACTTT-----GACTACTGGGGCCAAGTGACCACGGTCACCGTC348
			:::::
	Qy	168	SerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleGlu187
			:::::
	Db	349	TCCTCAGGTGGAGCGGTTTCAGCGGAGTTGGCTCTGGCGGTGGCGGATCGGACATCGAG408
			:::::
	Qy	188	LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArGAlaThrlleSerCys207
			:::::
	Db	409	CTCAGCTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGAGTCCACATGACCTGC468
			:::::
	Qy	208	ArgAlaSerGluSerValAspSerTyrrGlyAspSerPheMetHisTrpTyrrGlnGlnLys227
			:::::
	Db	469	AGTGCCAGCTCAAGTATA-----AGTTACATGCATCGGTATCATCAGCAAG513
			:::::
	Qy	228	ProGlyGlnProProLysLeuLeuIleTyrrArgAlaSerAsnLeuGluSerGlyValPro247
			:::::
	Db	514	CCAGGCACCTCCCCAAAAGATGGATTTTAGACACATCCAAACTGGGTCTCTGGAGTCCCT573
			:::::
	Qy	248	AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrlleAapProValGlu267
			:::::
	Db	574	GCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCAAAATCAGCAGCATGGAG633
			:::::
	Qy	268	GluAspAspAlaAlaValTyrrTyrrCysLeuGlnSerMetGluAspProTyrrThrPheGly287
			:::::
	Db	634	GCTGAAGATGCTGCCACTATTACTTGCCATCAGCGGAGTAGTTACCCATTACAGTTCGGA693
			:::::
	Qy	288	GlyGlyThrLysLeuGluIleLys295
			:::::
	Db	694	GGGGGGGCCAAGCTGGAAATAAAA717

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RESULT 11
US-10-749-522-5
; Sequence 5, Application US/10749522
; Publication No. US20050089510A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: AGENTS AND COMPOSITIO
; TITLE OF INVENTION: AND/OR TREATING OR P
; FILE REFERENCE: SOLOMON-2B
; CURRENT APPLICATION NUMBER: US/10/749,522
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-749-522-5

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Alignment Scores:	
Pred. No.:	7,198-78
Score:	935.50
Percent Similarity:	81.85%
Best Local Similarity:	72.98%
Query Match:	54.23%
DB:	21
Length:	717
Matches:	181
Conservative:	22
Mismatches:	36
Indels:	9
Gaps:	3

US-10-089-278-6 (1-329) x US-10-749-522-5 (1-717)

Qy	48	GluValIysLeuGlnGlnSerGlyAlaGluIeuValArgProGlyValSerVallysIle	67
	:		
	:		
Db	1	CAGCTCAAACTGCAGGAGTCAAGGGCTGAGCTGGTGAGCGCTCGGGGTCTCACTGAAGATT	60
Qy	68	SerCysIysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTyrVallysGlnSer	87
	:		
	:		
Db	61	TCCTGCAAGGGTTCGGCTACACATTCACTGATTATGCTATGCACTGGGTGAAGCAGAT	120
Qy	88	HisAlaIysSerLeuGluTyrIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr	107
	:		
	:		
Db	121	CATGCAAAAGCTTAGAGTGGAATGGAGTTATTAGTACTTACTATGGTGATGCTAGCTAC	180
Qy	108	AsnGlnArgPheIysGlyIysAlaThrMetThrValAspIysSerSerAsnThrAlaTyr	127
	:		
	:		
Db	181	AACCAAGAATTCAAGGGCAGGCCACAAATGACTGTAGACAAATCTCCAGCACGCTAT	240
Qy	128	LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp	147
	:		
	:		
Db	241	ATGGAACTTGCACAGACTGACATCTGAGGATTCGCCATCTATTACTGTGCCAAGAGGG	297
Qy	148	GlyAsnTyrGlyTyrTyrTyrAlaIeuAspTyrTyrGlyGlnGlyThrThrValThrVal	167
	:		
	:		
Db	298	GCTACTATGCTACTTT-----GACTACTGGGGCCAAAGTACACACGGTCAACGCTC	348
Qy	168	SerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlySerAspIleGlu	187
	:		
	:		
Db	349	TCCTCAGGTGAGCGGTTCAAGCGGAGTTGGCTCTGGCGGTGGCGGATCGGACATCGAG	408
Qy	188	LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSerCys	207
	:		
	:		
Db	409	CTCACTAGCTCCAGCAATCTGACTCTCCAGGGGAGAGGTCAACATGACCTGC	468
Qy	208	ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLys	227

Db 469 AGTGGCAGCTCAAGTATA-----AGTTACATGCACTGGTATACAGCAGAG 513
Qy 228 ProGlyClnProProLysLeuLeuLeuTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db 514 CCAGGCACCTCCCCCAAGAGATGATTTATGACACATCCAACTGGCTTCTGGAGTCCCT 573
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db 574 GCTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTATTTCTCTCAATCAGCAGCAGTGGAG 633
Qy 268 GluAspAlaAlaValTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 634 GCTGAAGATGCTGCCACTTATTTACTGCCATCAGCGGAGTAGTTACCATTCACGTTCCGA 693
Qy 288 GlyGlyThrLysLeuGluLeuLys 295
Db 694 GGGGGGGCCCAAGCTGGAAATATAAA 717

RESULT 12
US-11-073-526-5
; Sequence 5, Application US/11073526
; Publication No. US20050152878A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON-2C
; CURRENT APPLICATION NUMBER: US/11/073,526
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/830,954
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
; OTHER INFORMATION:
US-11-073-526-5

Alignment Scores:
Pred. No.: 7,19e-78 Length: 717
Score: 935.50 Matches: 181
Percent Similarity: 81.85% Conservative: 22
Best Local Similarity: 72.98% Mismatches: 36
Query Match: 54.23% Indels: 9
DB: 24 Gaps: 3

US-10-089-278-6 (1-329) x US-11-073-526-5 (1-717)

Qy 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
Db 1 CAGGTCAACTGCAGGAGTCAGGGGCTGAGCTGGTGGGCTCTGGGTCTCAGTGAAGATT 60
Qy 68 SerCysLysGlySerGlyTyrThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 61 TCCTGAAGGGTTCTGGCTACACATTACCTGATTATGCTATGCACTGGGTGAAGCAGAGT 120
Qy 88 HisAlaLysSerLeuGluTrpLleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107

Db 121 CATGCAAGAGCTAGAGTGGATTGAGTATTAGTACTTACTATGATGCTAGCTAC 180
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 181 AACCAAGAGTTCGAAGGCCAAGCCCAATGACTGTAGACAAATCCTCCAGCACAGCCTAT 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaAspSerAsp 147
Db 241 ATGGAACTTGCACAGATGACATCTGAGGATTCGCCATCTATTACTGTGCAAGAGG- 297
Qy 148 GlyAsnTyrGlyTyrTyrAlaLeuAspTyrTyrGlyClnGlyThrThrValThrVal 167
Db 298 GCTACTATGCTCTACTTT-----GACTACTGGGGCCCAAGTACCACGGTCCCGTC 348
Qy 168 SerSerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleGlu 187
Db 349 TCCTCAGGTGGAGCGGTTTCAGGCGGAGTTGGCTCTGGCGGTGGCGGATCGGACATCGAG 408
Qy 188 LeuThrGlnSerProSerSerLeuAlaValSerLeuGlyClnArgAlaThrIleSerCys 207
Db 409 CTCACCTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACATGACCTGC 468
Qy 208 ArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGlnLys 227
Db 469 AGTCCAGCTCAAGTATA-----AGTTACATGCACTGGTATCAGCAGAG 513
Qy 228 ProGlyGlnProProLysLeuLeuLeuTyrArgAlaSerAsnLeuGluSerGlyValPro 247
Db 514 CCAGGCACCTCCCCCAAGAGATGATTTATGACACATCCAACTGGCTTCTGGAGTCCCT 573
Qy 248 AlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProValGlu 267
Db 574 GCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTTCTCTCAATCAGCAGCAGTGGAG 633
Qy 268 GluAspAlaAlaValTyrCysLeuGlnSerMetGluAspProTyrThrPheGly 287
Db 634 GCTGAAGATGCTGCCACTTATTTACTGCCATCAGCGGAGTAGTTACCATTCACGTTCCGA 693
Qy 288 GlyGlyThrLysLeuGluLeuLys 295
Db 694 GGGGGGGCCCAAGCTGGAAATATAAA 717

RESULT 13
US-09-742-693-27
; Sequence 27, Application US/09742693
; Patent No. US20020019324A1
; GENERAL INFORMATION:
; APPLICANT: HOWELL, Steven
; APPLICANT: LITTLE, Julie C.
; APPLICANT: VAN DER LOGT, Cornelis P.
; APPLICANT: PARRY, Neil J.
; TITLE OF INVENTION: METHOD OF TREATING FABRICS
; FILE REFERENCE: C7536 (V)
; CURRENT APPLICATION NUMBER: US/09/742,693
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: EP99310431.4
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-742-693-27

Alignment Scores:
Pred. No.: 1,16e-77 Length: 996
Score: 935.00 Matches: 193
Percent Similarity: 72.39% Conservative: 22
Best Local Similarity: 64.98% Mismatches: 46

Qy 287 GlyGlyGlyThrLysLeuGluLeuLysArg 296
Db 715 GGTGGAGGCACCAAGCTGGAAATCAAAACGG 744

RESULT 15

US-10-610-452-13
; Sequence 13, Application US/10610452
; Publication No. US20050074855A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl
; APPLICANT: George D. Yancopoulos
; TITLE OF INVENTION: Cytokine-Specific Fusion Proteins and
; TITLE OF INVENTION: Therapeutic and Diagnostic Methods For Use
; FILE REFERENCE: REG 203E
; CURRENT APPLICATION NUMBER: US/10/610,452
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US9/22045
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1999-09-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 744
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-610-452-13

Alignment Scores:

Pred. No.:	1.43e-77	Length:	744
Score:	932.50	Matches:	180
Percent Similarity:	82.40%	Conservative:	26
Best Local Similarity:	72.00%	Mismatches:	41
Query Match:	54.06%	Indels:	3
DB:	21	Gaps:	2

US-10-089-278-6 (1-329) x US-10-610-452-13 (1-744)

Qy 48 GluValLysLeuGlnSerGlyAlaGluLeuValArgProGlyValSerValLysIle 67
Db 1 CAGGTCCAGCTTCAGCAGCTCGGGCTGAACCTGGCAAACTGGGGCCTCAGTGAAGATG 60
Qy 68 SerCysLysGlySerGlyThrPheThrAspTyrGlyMetSerTrpValLysGlnSer 87
Db 61 TCCTGCAAGGCTTCGGCTACACCTTACTAGCTACTGGATGCACTGGATATAACACAGAGG 120
Qy 88 HisAlaLysSerLeuGluTrpIleGlyLeuIleSerThrTyrTyrGlyAspProSerTyr 107
Db 121 CCTGGACAGGCTCGAATGGATTGGATACATTAACTCTAGCCTAGCCTGGTATACAGAGTAC 180
Qy 108 AsnGlnArgPheLysGlyLysAlaThrMetThrValAspLysSerSerAsnThrAlaTyr 127
Db 181 AATCAGAAGTTCAAGGACCAAGGCCACATTGACTGCACAGAAATCTCCAGCACAGCCTAC 240
Qy 128 LeuGluLeuAlaArgLeuThrSerGluAspSerAlaIleTyrTyrCysAlaArgSerAsp 147
Db 241 ATGCAACTGAGCGCTGACATCTGAGGACTCTGCAGCTCTATTACTGTGCAAGGGAC--- 297
Qy 148 GlyAsnTyrGlyTyrTyrTyrAlaLeuAspTyrTrpGlyGlnGlyThrThrVal 167
Db 298 ---TACTATGATTACCAAGATGTTATGGACTACTGGGGTCAAGGAACCTCAGTCAACGTC 354
Qy 168 SerSer---GlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerAspIle 186
Db 355 TCCTCAGCGGTGGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATT 414
Qy 187 GluLeuThrGlnSerProSerLeuAlaValSerLeuGlyGlnArgAlaThrIleSer 206

Db 415 GTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATCTCC 474
Qy 207 CysArgAlaSerGluSerValAspSerTyrGlyAspSerPheMetHisTrpTyrGlnGln 226
Db 475 TGCAGAGCCAGCGAAAGTGTGTGATGGTTTGGCAATTAGTTTATGAACGTGTTCCAACAG 534
Qy 227 LysProGlyGlnProProLysLeuLeuIleTyrArgAlaSerAsnLeuGluSerGlyVal 246
Db 535 AAACCAAGGACAGCCCAACCTCTCATCTATGCTGCATCCCAACCAAGGATCGGGGTC 594
Qy 247 ProAlaArgPheSerGlySerGlySerGluSerAspPheThrLeuThrIleAspProVal 266
Db 595 CCTGCCAGGTTTAGTGGCAGTGGTCTGGGACAGACTTCAGCCTCAACATCCATCTCTATG 654
Qy 267 GluGluAspAlaAlaValTyrTyrCysLeuGlnSerMetGluAspProTyrThrPhe 286
Db 655 GAGGAGGGTGATGCTGCAATGATTCTCTCAGCAAAATTAAGGAGGTTCGTTGGACGTTT 714
Qy 287 GlyGlyGlyThrLysLeuGluIleLysArg 296
Db 715 GGTGGAGGCACCAAGCTGGAAATCAAAACGG 744

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Job time : 8184 secs

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